

|                |  |      |        |
|----------------|--|------|--------|
|                | Kupffer cell receptor                                    |      |        |
|                | secretory phospholipase A2 receptor                      |      |        |
|                | secretory phospholipase A2 receptor                      |      |        |
|                | asialoglycoprotein receptor                              |      |        |
|                | mannose receptor   |      |        |
|                | aggrin alpha 1 chain                                     |      |        |
|                | agkisacutacin beta                                       |      |        |
|                | phospholipase A2 receptor                                |      |        |
|                | Ly-49G.2 antigen -                                       |      |        |
|                | Ly-49G.1 antigen -                                       |      |        |
|                | chondroitin sulphatase                                   |      |        |
|                | phospholipase A2 receptor                                |      |        |
|                | pancreatitis-associated protein                          |      |        |
|                | pancreatic stoneman                                      |      |        |
|                | natural killer cell scavenger receptor                   |      |        |
| 3.0            | 148.5  | 14.5 | 550    |
| 3.1            | 146.5  | 14.3 | 1326   |
| 3.2            | 146.5  | 14.3 | 1465   |
| 3.3            | 146  | 14.3 | 311    |
| 3.4            | 145.5  | 14.2 | 1479   |
| 3.5            | 143.5  | 14.0 | 144    |
| 3.6            | 142  | 13.9 | 146    |
| 3.7            | 141.5  | 13.8 | 1458   |
| 3.8            | 140.5  | 13.7 | 267    |
| 3.9            | 140.5  | 13.7 | 280    |
| 4.0            | 139.5  | 13.6 | 3562   |
| 4.1            | 138.5  | 13.5 | 1463   |
| 4.2            | 137.5  | 13.4 | 175    |
| 4.3            | 137  | 13.4 | 165    |
| 4.4            | 137  | 13.4 | 266    |
| 4.5            | 137  | 13.4 | 149363 |
|                | US-09-811-3670-1   |      | JC7595 |
| perfect score: | 1023   |      |        |
| sequence:      | 1 MFTDSVIYSMMLPPTAQAN . . . . . GLQASSCEVPLHGVCKVKRL 189 |      |        |
| oring table:   | BIGSSTIME62  |      |        |

searched: 283366 seqs, 96191526 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

```
1: pir1: *
```

3: ~~pir3:~~

ered. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, *assuming that the distribution of the scores is uniform*.

COMMUNES

A;Residues: 1-225 &lt;RES&gt;

A;Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PMID:9544496

C;Superfamily: natural killer cell receptor P1; C-type lectin homology F;94-210/Domain: C-type lectin homology &lt;LCH&gt;

Query Match 19.6% Score 201; DB 2; Length 225;

Best Local Similarity 26.0%; Pred. NO. 1.7e-11;

Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

A;Status: preliminary

A;Molecule type: mRNA

A;Accession: A46467

A;Residues: 'MHLCT' ,1-227 &lt;GI0&gt;

A;Cross-references: GB:M77676; NID:9200058

A;Experimental source: A-LNK cells, C57BL

A;Note: sequence extracted from NCBI backbone (NCBIN:52379); the sequence

R;Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.

J. Immunol. 149, 1957-1963, 1992

A;Title: Genomic structure and strain-specific expression of the natural killer cell receptor gene

A;Reference number: A46502; MUID:92388663; PMID:1517565

A;Accession: A46502

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-109, 'H', 111-181, 'D', 183-227 &lt;GI2&gt;

A;Cross-references: GB:X64116; NID:953395; PIDN:CAA45971.1; PMID:917989

A;Experimental source: BALB/c 3T3 fibroblastoid cell line

A;Note: sequence extracted from NCBI backbone (NCBIN:113037; NCBIN:113063; NCBIN:113072)

R;Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.

J. Immunol. 147, 3229-3236, 1991

A;Title: cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of

A;Reference number: A46456; MUID:92013158; PMID:1680927

A;Accession: A46456

A;Molecule type: mRNA

A;Residues: 1-38, 'I', 40-227 &lt;YOK&gt;

A;Cross-references: GB:M77553; NID:919856; PIDN:AAA39366.1; PMID:9198570

A;Note: sequence extracted from NCBI backbone (NCBIN:60329; NCBIP:60431)

C;Superfamily: natural killer cell receptor P1; C-type lectin homology

F;94-210/Domain: C-type lectin homology &lt;LCH&gt;

Query Match 18.7% Score 191; DB 2; Length 227;

A;Best Local Similarity 27.4%; Pred. NO. 1.5e-11; Mismatches 43; Indels 16; Gaps 7;

A;Conservative 49; Matches 49; Score 191; DB 2; Length 227;

Qy 24 PQKSSSSKPSCSCLVAITGLL-TAVILSLLYQ-----WILCQGS-NYST-CASPS 74

Db 34 PRSHRSALKSPAGLILUVVVLIGMSVLLQVKPLSTEKCVLQVNINKTDCSASKL 93

A;Cross-references: GB:CDPWWXGNHCVYFSVEKDWNSSLEFLCLARDSHLWITDNOEMSLLQVF 75

A;Superfamily: C-type lectin homology

F;129-241/Domain: C-type lectin homology &lt;LCH&gt;

Db 94 CPQDWLSHRDKCFHVQSNTWEGLYVDCDGKATMLQDQEELRLDSIKEKNSFW 153

Qy 133 TGLR--NNSGCWWDGSPINES--RISSNSFVQTGCAGAKNGLQASSCEYPLHGCK 196

Db 154 IGLRTLPDNWKWINGSTNSDVAISGDKVTFESCNSDNRWTCQK 212

RESULT 5

Db 64 EATTREGDEERSQRGGCSELRQNRRRVLVCAVASPCMLVLAVALVIVQPS---C 119

PT0372 natural killer cell receptor group 2, splice form A - human

N;Alternate names: NKG2-A; NKG2-B

N;Contains: natural killer cell receptor group 2, splice form B

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence\_change 31-Mar-1992

C;Accession: PT0372; PT0373

R;Houchmandzadeh, B.; Yabe, T.; McSherry, C.; Bach, F.H.

J. Exp. Med. 173, 1017-1020, 1991

A;Title: DNA sequencing of NKG2, a family of related cDNA clones encoding type I

A;Reference number: PT0372; MUID:91178434; PMID:2007850

A;Accession: PT0372

A;Molecule type: mRNA

A;Residues: 1-233 &lt;HOUL&gt;

A;Cross-references: EMBL:X54867; NID:935056; PIDN:CAA38649.1; PMID:935057

A;Experimental source: natural killer cell

A;Accession: PT0373

A;Molecule type: mRNA

A;Residues: 1-95, 114-233 &lt;HOUL&gt;

A;Cross-references: GB:54868; NID:935058; PIDN:CAA38650.1; PMID:935059

A;Experimental source: natural killer cell

C;Genetics:

A;Gene: GDB:KLRCL; NKG2

RESULT 4

A;Residues: 1-233 &lt;HOUL&gt;

A;natural killer cell receptor P1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence\_change 19-Feb-1999

C;Accession: A46467; A46502; A46456

R;Giorda, R.; Trucco, M.

A; cross-references: GDB:138773; OMIM:161555  
 A; Map position: 12pter-12qter  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 C; Keywords: alternative splicing; glycoprotein; transmembrane protein  
 F; 71-98/Domain: transmembrane #status predicted <TRA>  
 F; 102,103,157,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 119-130,147-229,208-221/Disulfide bonds: #status predicted  
 Query Match Score 18.6%; Best Local Similarity 27.8%; Length 233;  
 Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;  
 QY 5 VIVSMLEPTATQAOQNDYGPQQKSSSK--PSC-SCLVAVITGLLTAVIL---SVLYQ 57  
 Db 38 ITYARLNQKASQ--DFQENDKTYTHCKDLPSPAEKLIGLICLIMASVVTIVTP 94  
 QY 58 WILCGNSYST-----CASCPCPDRMKYGNHCYYSVEEKDWNSSLEFLARDSHL 110  
 Db 95 STLQRHNNSSLNTRTQARHCGRGCPPEWVITYNSNCYTIGKERSTWEELLAUTSKNSL 154  
 QY 111 LVTIDNQENSLLQLQVLFSEAFCWIGL-RNNSGWRPEDGSSLINFSR--ISSNSFVOTCGAIN 167  
 Db 155 LSIDNEEKKFLSISPPS--WIGYFRNSHHHPWYTMNGLAFKHEIKDSDNAELNCAVIL 212  
 Qy 168 KNGQIASSCEVPLGVCK 185  
 Db 213 VNRLKSAQCSSIIYHCK 230  
 RESULT 6  
 natural killer cell receptor group 2-C, splice form 1 - human  
 N; Alternate names: NKG-C  
 C; Species: Homo sapiens (man)  
 C; Accession: PT0374  
 C; Revision: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 19-May-2000  
 R; Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.  
 J. Exp. Med. 173, 1017-1020, 1991  
 A; Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II  
 A; Reference number: PT0372; MUID:91178434; PMID:2007450  
 A; Accession: PT0374  
 A; Molecule type: mRNA  
 A; Residues: 1-231 <HOU>  
 A; Experimental source: natural killer cell  
 A; Cross references: GDB:X54869; NID:935060; PIDN:CAA38651.1; PID:935061  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 C; Keywords: glycoprotein; transmembrane protein  
 F; 71-96/Domain: transmembrane #status predicted <TRA>  
 F; 27,100-149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match Score 17.8%; Best Local Similarity 27.8%; Length 231;  
 Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;  
 QY 24 PQQKSSSSPKPSCSCLVAVITGLLTAVIL---CASCPCPDRW 79  
 Db 67 PPEKLTAEVLGICIV----LMATVLRKTVLIPBLEQNNSPNTRTQARHCHCPEPW 121  
 QY 80 MKYGNHCYYSVEEKDWNSSLEFLARDSHLVLVTDNQMSLQLQVLFSEAFCMGL-RN 138  
 Db 122 ITYNSCYTIGKERSTWEELLAUTSKNSLSDNEEIKFLASTILPS--WGVFRNS 179  
 QY 139 SGWRWEDGSPNFSR--ISSNSFVOTCGAINKGQASSCEVPLRGVCK 185  
 Db 180 SHHPWVTINGLAFKHKIXOSDNAAELNCAVILQVNRLKSACQGSSMIYHCK 228  
 RESULT 5  
 natural killer cell receptor group 2-D - human  
 N; Alternate names: integral membrane protein NKG2-D  
 C; Species: Homo sapiens (man)  
 C; Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-May-2000  
 R; Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.  
 J. Exp. Med. 173, 1017-1020, 1991  
 A; Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type I  
 A; Reference number: PT0372; MUID:91178434; PMID:2007450  
 A; Accession: PT0375  
 A; Molecule type: mRNA  
 A; Residues: 1-216 <HOU>  
 A; Cross references: EMBL:X54870; NID:935062; PIDN:CAA38652.1; PID:935063  
 C; Experimental source: natural killer cell  
 A; Note: translation of nucleotide sequence is not complete  
 C; Keywords: transmembrane protein  
 Query Match Score 18.0%; Best Local Similarity 26.8%; Pred. No.: 1.6e-09;  
 Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;  
 QY 37 CLVAITLG-----ILTAVILSVLQYOWTLCOGGNSYSTACSPSCPDRMKYGNHCYX 88  
 Db 57 CTFIAVAMGIRFTIMVAVSFVNSLNFNQEVLQP----LTTESGCPKPKNWICYKNKNYQ 112  
 QY 89 FSVTEKDWSLSSLEFLARDSHLVLVTDNQMSLQLQVLFSEAFCMGL--RNNSGTRWED 145  
 Db 113 FFDDESKNYYEQASCMSQNASLKVSKSDEDQDLIK--LVKSYHWMGLVHPIPTGSQWED 170  
 QY 146 GSPINFSR-----SSNSFVQTCCAIN 167  
 Db 171 GSTISPNLITIEMQKDCAIYASSFKHIEQNSTPN 207  
 RESULT 8  
 natural killer cell receptor group 2-C, splice form 2 - human  
 N; Alternate names: NKG-C  
 C; Species: Homo sapiens (man)  
 C; Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 19-May-2000  
 R; Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.; Houchins, J.P.  
 Immunogenetics 39, 218, 1994  
 A; Title: Natural killer cell lectin-like receptors have divergent carboxy-termini, distinct  
 A; Reference number: 154524; PMID:94102823; PMID:8276468  
 A; Accession: 154524  
 A; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: mRNA  
 A; Cross references: GB:L14542; NKG2-C  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Experimental source: natural killer cell  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>  
 A; Cross references: GDB:9787095  
 A; Molecule type: mRNA  
 A; Accession: PT0374  
 A; Map position: 12p13-12p13  
 C; Superfamily: natural killer cell receptor P1; C-type lectin homology  
 A; Residues: 1-231 <HOU>

|   |   |  |
|---|---|--|
| RESULT 9  |   |  |
| A46274  | HIV gp120-binding C-type lectin - human                     |  |
| C;Species: Homo sapiens (man)   |   |  |
| C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995   |   |  |
| C;Accession: A46274   |   |  |
| R;Curtis, B.M.; Scharnowski, S.; Watson, A.J.   |   |  |
| Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992   |   |  |
| A;Title: Sequence and expression of a membrane-associated C-type lectin that exhibits   |   |  |
| A;Reference number: A46274; PMID:1518869  |   |  |
| A;Accession: A46274   |   |  |
| P;Status: Preliminary   |   |  |
| N;Molecule type: nucleic acid   |   |  |
| A;Residues: 1-404 <CIR>   |   |  |
| A;Experimental source: placenta   |   |  |
| A;Note: sequence extracted from NCBI backbone (NCBIP:113134, NCBIP:113135)  |   |  |
| C;Superfamily: C-type lectin homology   |   |  |
| F;256-377/Domain: C-type Lectin homology <LCH>  |   |  |
| Query Match Score 17.2%; Best Local Similarity 30.7%; Matches 39; Conservative 23; Mismatches 53; Indels 12; Gaps 5;  |   |  |
| Qy 72 CPSCPDMMKYGHNYCYFSVEEKDNNSLEFCLARDSHLYITTDQMSLQVLFSEA-- 129   |   |  |
| Db 253 CHCPWPWTFTEQQNCYPMNSGRNWDHSITACKEVGAGQLQVVIKSAAEIQNFQLOQSSRSNR 312   |   |  |
| Qy 130 FWMGLR--NNNG-WRVEDGSPL--NFSRI----SSNSFVQTGAINKGQIQAASSCEVP 179   |   |  |
| Db 313 FWMGLSDLNQESTWQWDGSPLLPSPKQYWRGEPEPNVGEDCAEEPSGNGNDKCNLA 372   |   |  |
| Qy 180 LHGVCK 186   |   |  |
| Db 373 KFWICK 379   |   |  |
| RESULT 10   |   |  |
| A35917  | NK-cell receptor P1 - rat                                   |  |
| C;Species: Rattus norvegicus (Norway rat)   |   |  |
| C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999   |   |  |
| C;Accession: A35917   |   |  |
| R;Giorda, R.; Rudert, W.A.; Varassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.   |   |  |
| A;Title: NKR-P1, a signal transduction molecule on natural killer cells.  |   |  |
| A;Reference number: A35917  |   |  |
| A;Status: preliminary   |   |  |
| A;Molecule type: mRNA   |   |  |
| A;Residues: 1-223 <G10>   |   |  |
| A;Cross-references: GB:M62891; PID:9205722; PID:AAA41710.1; PID:9205723   |   |  |
| C;Superfamily: natural killer cell receptor Pi; C-type lectin homology  |   |  |
| F;94-210/Domain: C-type Lectin homology <LCH>   |   |  |
| Query Match Score 17.2%; Best Local Similarity 27.1%; Matches 44; Conservative 44; Mismatches 67; Indels 21; Gaps 9;  |   |  |
| Qy 24 PQQRSSSRPSCSCLVATLGLL-TAVILSVLYQ-----WILCGSSNYSTCASCSCS-- 74  |   |  |
| Db 35 PRSHRLAKLKLSCAGLILVILVLMGMSLILVRLVQKPSVEPCRVLQ-ENLSKTGS-PAKL 92   |   |  |
| Qy 75 -CPDRWKKYGNHNYCYFSVEEKDNNSLEFCLARDSHLYITTDQMSLQVLFSEA-- 130   |   |  |
| Db 93 KCPKDWWLSDRDKCFHVSYTSITWKESLADGGKGATLILVQDQEELTRFLRNLTKRSSSF 152  |   |  |
| Qy 131 CWIGLR--NNNGWRVEDGSPLNFS--RISNSFVQTGAINKGQIQAASSCEVPHGCVK 185  |   |  |
| Db 153 -WIGLSYTLSDENWKWINGSTLNSDVLSITGDEKDSASVSDQKVLSSECDSDNTWVCQ 211   |   |  |
| Qy 186 K 186  |   |  |
| RESULT 11   |   |  |
| JX0209  | JX0209 galactose/N-acetylgalactosamine-specific - mouse     |  |
| C;Species: Mus musculus (house mouse)   |   |  |
| C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999   |   |  |
| C;Accession: JX0209; PX0009   |   |  |
| R;Sato, M.; Kawakami, K.; Osaka, T.; Toyoshima, S.  |   |  |
| J. Biochem. 111, 331-336, 1992  |   |  |
| A;Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylgalactosamine-specific lectin, galactose/N-acetylgalactosamine-specific - mouse                      |   |  |
| A;Reference number: JX0209; MUID:92268032; PMID:1587794   |   |  |
| A;Accession: JX0209   |   |  |
| A;Molecule type: mRNA   |   |  |
| A;Residues: 1-304 <SAT>   |   |  |
| A;Cross-references: GB:S36676; PID:9249360; PID:AAB22171.1; PMID:9249361  |   |  |
| R;Oda, S.; Sato, M.; Toyoshima, S.; Osaka, T.   |   |  |
| J. Biochem. 104, 100-105, 1988  |   |  |
| A;Title: Purification and characterization of a lectin-like molecule specific for galactose/N-acetylgalactosamine-specific lectin, galactose/N-acetylgalactosamine-specific - mouse |   |  |
| A;Reference number: PX0009; MUID:89197865; PMID:3241002   |   |  |
| A;Accession: PX0009   |   |  |
| A;Molecule type: protein  |   |  |
| A;Residues: 102-120:137'X',119-151 <ODA>  |   |  |
| C;Superfamily: hepatic lectin, C-type lectin homology   |   |  |
| C;Keywords: glycoprotein; lectin; macrophage; transmembrane protein   |   |  |
| F;36-61/Domain: transmembrane #status predicted <TRA>   |   |  |
| F;173-296/Domain: C-type lectin homology <LCH>  |   |  |
| F;74-166/Banding site: carbohydrate (Asn) (covalent) #status predicted  |   |  |
| Query Match Score 17.1%; Best Local Similarity 27.5%; Length 304; Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;  |   |  |
| Qy 59 IICQGSNYSCTAS-CPSCPDMMKYGHNYCYFSVEEKDNNSLEFCLARDSHLYITTDQMSLQVLFSEA-- 117   |   |  |
| Db 156 ITCQLANLKNGNSEVACCPLHTEHEGSCYWPSESEKSWPDAKYCRLENSHLVYVNSLE 215   |   |  |
| Qy 118 EMSLLOVLFSEAFCWIGLRRNNSG-WRVEDGSPL---NFSRISNSNSFV----NFSRISNSNSFV---- 185  |   |  |
| Db 216 BONFLQRNLANYVSWIGLTDONGPWRVDFEGKFKENWAPLQDPDNWFHGHLGGGEDCA 275   |   |  |
| Qy 165 AINKNG-LQASSECVPLHGVCK 185   |   |  |
| Db 276 HTTGGPWNDDYCORTRFWICE 297  |   |  |
| RESULT 12   |   |  |
| JH0822  | JH0822 lymphocyte early activation antigen AIM/CD69 - human |  |
| C;Species: Homo sapiens (man)   |   |  |
| C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999   |   |  |
| C;Accession: JH0822; S60753   |   |  |
| R;Lopez-Cabreria, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M  |   |  |
| J. Exp. Med. 178, 537-547, 1993   |   |  |
| A;Title: Molecular cloning, expression, and chromosomal localization of the human early   |   |  |
| mitting receptors.  |   |  |
| A;Reference number: JH0822; MUID:93340630; PMID:8340758   |   |  |
| A;Accession: JH0822   |   |  |
| A;Molecule type: mRNA   |   |  |
| A;Residues: 1-199 <LGP>   |   |  |
| A;Cross-references: GB:Z22576; PID:CAAB0298.1; PID:9397939  |   |  |
| R;Hamann, J.; Fleibig, H.; Strauss, M.  |   |  |
| J. Immunol. 150, 4920-4927, 1993  |   |  |
| A;Title: Expression cloning of the early activation antigen CD69, a type II integral mem  |   |  |
| A;Reference number: I56167; MUID:93267093; PMID:8496594   |   |  |
| A;Accession: I56167   |   |  |
| A;Status: translated From GB/EMBL/DBJ   |   |  |
| A;Molecule type: mRNA   |   |  |
| A;Residues: 1-199 <RES>   |   |  |
| A;Cross-references: GB:L0755; PID:9291897   |   |  |
| R;Santis, A.G.; Lopez-Cabreria, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.   |   |  |

Bur. J. Immunol. 24, 1692-1697, 1994  
 A;Title: Structure of the gene coding for the human early lymphocyte activation antigen receptors.  
 A;Reference number: S60753; MUID:94298875; PMID:8026529  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:230426; NID:9525242; PIDN:CAA83017\_1; PID:G558352  
 C;Comment: This protein is the earliest inducible cell surface glycoprotein expressed in  
 A;Gene: GDB:CD65  
 A;Cross-references: GDB:132925; OMIM:107273  
 A;Map position: 12p1.3-12p1.2  
 C;Superfamily: C-type lectin homology  
 C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
 F;39-64/Domain: transmembrane #status predicted <TMM>  
 F;85-194/Domain: C-type lectin homology <LCH>  
 F;18-30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted  
 F;165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 174; DB 2; Length 199;  
 Best Local Similarity 22.9%; Pred. No. 5.e-09;  
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

Qy 30 SSKPCSCVAVITLGILTVAVLISVLYQNTLCOGSNYSCTACSP-----SC 75  
 Db 30 STRHEGSFQVPVLCAVNNTFVITLIALIALSNGVQY---NCPGQYTTSMPSDSHVSSC 85  
 Qy 76 PDRMKYGHCCYYFSVEEEKWDNASSLEFCIARDSHLLIVTDNQEMSLIQVFLSERFCWTGL 135  
 Db 86 SEDDVGYQRCYCFISTVRSWTSQAONACESEHGATLAVISEKDNFLKXYAGREHHWYGL 145  
 Qy 136 RNNSSG-WRWEDEGSPLN--FSRISNSFVYQTCGAINKNGQASSECVPHGVCK 186  
 Db 146 KKEPSPHWKWSNGKEFENNWFNVTGSDK---CVFLKNTTEVSSMECEKNLYWICNK 196

## RESULT 13

JC7608 type II lectin-like immunoreceptor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001  
 C;Accession: JC7608  
 R;Huang, X.; Yuan, Z.; Chen, G.; Zhang, M.; Zhang, W.; Yu, Y.; Cao, X.  
 Bichem. Biophys. Res. Commun. 281, 131-140, 2001  
 A;Title: Cloning and characterization of a novel ITIM containing lectin-like immunorecep  
 A;References: JCR608; MUID:1117897; PMID:121092797;  
 A;Comments: Dendritic cells  
 A;Accession: JC7608  
 A;Molecule type: mRNA  
 A;Cross-references: GB:AF067800  
 C;Comment: This receptor, highly homologous to the group of macrophage/hepatocyte lectins is  
 cell especially in migrating, antigen capturing and processing.  
 C;Genetics:

A;Gene: llir

A;Map position: 12p13  
 F;45-69/Domain: transmembrane #status predicted <TMM>

Query Match Score 16.5%; DB 2; Length 237;  
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;  
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

Qy 1 MTDSVIYSMEL-----PTATQAONDYGEQQKSSSKPSKSCSCLVAVITGLTAVL 50  
 Db 1 MTSETTYAFVRKFNEKSSGINTASSAAKERTAPLKNTGFPKLCLASLIFILLIAS 60

Qy 51 LSV-----LLYQWTLQCSNNY---STCASCSCPDRMKYGHCV 87

Db 61 FFIAFVIFPQKYSOLLEKRTKELVHTLECVRKNMPPVEETAWSC-CPKMKSFSSNCY 118

Qy 88 YFSVBEKKDNNSLLEFCIARDSHLLIVTDNQEMSLIQVFLSERFCWTGL 143

Db 119 F1STASASWDOSEKDFARMEAHLLIVTQEQEQQDFIFQNLQEESEAVFGLSDPEGGRHWW 178

Qy 144 EDGSPLNFSRISNSF-----VQTCGAIN----KNGLOSSCCEVPLHGCKKVR 188

Db 179 VDQRYN----ESSFWHPREPSSDENRCVULNFKSPKRKGWNWVNLGPQRTSCEMMK 244

Qy 189 L 189

Db 235 I 235

## RESULT 14

S13165 asialoglycoprotein receptor - mouse

N;Alternate names: hepatic lectin  
 C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 20-Aug-1999

C;Accession: S13165  
 R;Sanford, J.P.; Doyle, D.

Biochim. Biophys. Acta 1087, 259-261, 1990

A;Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene

F;170-295/Domain: C-type lectin homology <LCH>  
 A;Accession: S13165  
 A;Molecule type: mRNA  
 A;Residues: 1-301 <SAN>

A;Cross-references: EMBL:X53042; NID:953104; PIDN:CAA37211\_1; PMID:953105

C;SuperFamily: hepatic lectin; C-type lectin homology

C;Keywords: glycoprotein; liver; transmembrane protein

Query Match Score 16.3%; DB 2; Length 301;

Best Local Similarity 25.9%; Pred. No. 3.6e-08;  
 Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

Qy 27 KSSSSRPSSCLVAI---TGIGLTAVL-----SVLTY-----SVLTY-----56

Db 92 KETPSNFSSTIMEFGLDTLGTGSEKDTLWQLEEKQQQLKAHDSTLLFHJRHFPMD 151

Qy 57 -QWILCQ---GSNYSTCASCPCSPDRMKYGHCVYFSVEEKDNNSLLEFCIARDSHLL 111

Db 152 LRTITCQLAYFQSGNTEC----CPVANVEFGGSCYWFSSRDLGTWAEAOYCCOLENAHLL 206

Qy 112 VITDNEQNSLILQYFLSEAFCWIGLNGQAKNGQASSECVPHGVCK 161

Db 207 VINSREEQDFWVKGHRSPQHIFTGLDGSWQKWDGTDYR-SMYRNWAAFTQPDNWQHQEQ 265

Qy 162 ---TGGAAINKG-LQASSCEVPLHGCVKVR 188

Db 266 GGEBDCAAFLISDGHNDFCQQYMRWVCCR 297

## RESULT 15

T28141 C type lectin, B locus - chicken

C;Species: Gallus gallus (chicken)  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999

R;Milne, S.; Kaufman, J.; Beck, S.

submitted to the BMBL Data Library, May 1998  
 A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp

A;Accession: T28141  
 A;Reference number: 220475

A;Status: Preliminary; translated from GB/EMBL/DDBJ

A;Map position: 52; Conservation 39; Mismatches 92; Indels 58; Gaps 9;

Qy 1 MTDSVIYSMEL-----PTATQAONDYGEQQKSSSKPSKSCSCLVAVITGLTAVL 50

Db 1 MTSETTYAFVRKFNEKSSGINTASSAAKERTAPLKNTGFPKLCLASLIFILLIAS 60

Qy 51 LSV-----LLYQWTLQCSNNY---STCASCSCPDRMKYGHCV 87

Db 61 FFIAFVIFPQKYSOLLEKRTKELVHTLECVRKNMPPVEETAWSC-CPKMKSFSSNCY 118

A;Genetics:  
 A;Map position: 16  
 A;Introns: 17/1; 74/3; 110/2

|                    |                  |   |            |         |             |
|--------------------|------------------|---|------------|---------|-------------|
| Query              | Match            | 16.2%   | Score 166; | DB 2;   | Length 156; |
| Best Local Matches | Similarity 29.7% | Pred. No. 2.3e-08;  |            |         |             |
| Matches 46;        | Conservative 19; | Mismatches 68;  | Indels 22; | Gaps 5; |             |
| 2y                 | 42               | TGILDATVLLSIVYLQWLQCGSSNYTCASCPSCPDRWMKXGYFSVEEKDNNSLE 101          |            |         |             |
| Ddb                | 6                | TVLLITAVAFAYQAQF ----- PHPQPQCAQQCPFDWIGPRGKCYYPSEDBSNWTTSSQN 56    |            |         |             |
| 2y                 | 102              | FCLARDSHLLVITDNOEMSLLQVFLSEAFNCWIGRANNS -- GWRMEDGSPLNFSRISSSNS 158 |            |         |             |
| Ddb                | 57               | NCSALGASLAVFDSEAEDLSFTMRHGSSPHWGLSREGKEHPWEWNRSPU-----SHL 110       |            |         |             |
| 2y                 | 159              | F-YQ---TCGAINKNGHQASSCEVPLEGYCKVRL 189                              |            |         |             |
| Ddb                | 111              | POVQDGNDGICAYIGDAGI:SSSHESCTRRNWVCTKPAL 145                         |            |         |             |

Search completed: August 10, 2004, 16:19:35  
Job time : 13:0425 secs



|                       |   |
|-----------------------|---|
| DR                    | InterPro; IPR013104; Lectin_C.  |
| PFAM                  | PF00059; lectin_c; 1.   |
| DR                    | SMART; SM00134; CLECT; 1.   |
| DR                    | PROSITE; PS001615; C_TYPE_LECTIN_1; FALSE_NEG.  |
| DR                    | PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   |
| KW                    | Protein; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein; Alternative splicing; Polymorphism.                            |
| KW                    | CYTOSLIC (TYPE-I) MEMBRANE PROTEIN.   |
| FT                    | TRANSMEM 1 70 SIGNAL-ANCHOR (TYPE-II) MEMBRANE PROTEIN  |
| FT                    | TRANSMEM 71 93 (POTENTIAL).   |
| FT                    | DOMAIN 9 4 233 EXTRACELLULAR (POTENTIAL).   |
| FT                    | DOMAIN 118 231 C-TYPE LECTIN (LONG FORM).   |
| FT                    | DISULFID 119 130 BY SIMILARITY.   |
| FT                    | DISULFID 147 229 BY SIMILARITY.   |
| FT                    | DISULFID 208 221 BY SIMILARITY.   |
| FT                    | CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT                    | CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT                    | CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT                    | CARBOHYD 180 180 Missing (in isoform NKG2-B).   |
| FT                    | VARSPLIC 96 113 /FT1C=VSP 003066.   |
| FT                    | VARIANT 7 9 79 I -> L (in NKG2-A*03).   |
| FT                    | VARIANT 231 231 H -> R (in NKG2-A*03).  |
| SQ                    | SEQUENCE 233 AA; 26212 MW; AE34BEA2A0209984 CRC64;  |
| Query Match           | 19.5%; Score 199; DB 1; Length 233;   |
| Best Local Similarity | 28.4%; Pred. No. 6.7e-12;   |
| Matches               | 56; Conservative 34; Mismatches 87; Indels 20; Gaps 7;  |
| QY                    | 5 VIYSMELPLTATQ-AQNDYGPQQKSXPSSKPSCLAVITGLLTAVLL---SVIILYQW 58  |
| Db                    | 38 ITYALNLNOKASQDFQENDTYHCIDLPSAI--EKLIVGIGLICLILMASVVTIVIPS 95   |
| QY                    | 59 ILCCQGSNST----CASPSCPDRCRMXYGNHCCYFSVEEKDNNSLLEFLCLARDSHLI 111   |
| Db                    | 96 TLIQRHNNSSLNTRTOKARHGCHCPPEWTTYSNSCYIGKERRTVTEESLLACTSKNSGLL 155   |
| QY                    | 112 VITDQEMLSILQVESEAFCWIGL-RNNSGMRWEDSPLNSR--LSNSNVQTCAINK 168   |
| Db                    | 156 SIDNEEMKPLTSISPPS-WIGVFRNSSSHHPWTTINGLAFKHEIKDSDNAELNCAVLQV 213   |
| QY                    | 169 NGLQASSCEVPLHGYCK 185   |
| Db                    | 214 NGLKSAQCGSSTIYHCK 230   |
| RESULT 2              |   |
| CD94_MACMU            | STANDARD; PRT; 179 AA.  |
| ID                    | -CD94_MACMU   |
| AC                    | Q9MK9; Q9GK91; Q9MK27; Q9MZKB;  |
| DT                    | 28-FEB-2003 (Rel. 41; Created)  |
| DT                    | 28-FEB-2003 (Rel. 41; Last sequence update)   |
| DT                    | 10-OCT-2003 (Rel. 42; Last annotation update)   |
| DE                    | Natural killer cell antigen CD94 (NK cell receptor) (Killer cell  |
| DB                    | Lectin-like receptor subfamily D, member 1).  |
| GN                    | KLRL1 OR CD94.  |
| OS                    | Macaca mulatta (Rhesus macaque).  |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;   |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;   |
| OC                    | Cercopithecinae; Macaca.  |
| NCBIX_TAXID           | 9544;   |
| RN                    | [1] SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).   |
| RX                    | MEDLINE=20322487; PubMed=1086611;   |
| RA                    | LaBonte M.L.; Levy D.B.; Letvin N.L.;   |
| RT                    | "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D."; |
| RL                    | Immunogenetics 51:496-499(2000).  |
| RN                    | [2] SEQUENCE FROM N.A. (ISOFORM 1).   |
| RX                    | MEDLINE=21158386; PubMed=11261355;  |
| RA                    | Krawitz R.H.; Grendell B.R.; Shulkin I.I.; Golos T.G.;  |
| RT                    | "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative  |

RESULT 3

CD94 HUMAN STANDARD: PRT; 179 AA.

AC Q13241; 043321; 043773; Q9UBB2; QUBQ0;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DB Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1) (Kp43).

GN KLRD1 OR CD94.

OS Homo sapiens (Human).

OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI\_TaxID=9606;

RN [1] SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=BLOOD;

RX MEDLINE=96011848; PubMed=7589107;

RA Chang C., Rodriguez A., Carrasco M., Lopez-Botet M., Phillips J.H., Lanier L.L.; "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily.";

RN [2] SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=98139529; PubMed=9472066;

RA Rodriguez A., Carrasco M., Glienke J., Bellon T., Ramirez A., Lehrach H., Francis F., Lopez-Botet M.; "Structure of the human CD94 C-Type Lectin gene.";

RN [3] SEQUENCE FROM N.A. (ISOFORM 2).

RA Biassoni R.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN [4] SEQUENCE FROM N.A. (ISOFORM 3).

RA MEDLINE=98267245; PubMed=961951;

RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K., Tohma S., Inoue T., Yamamoto K., Juji T.; RT "A alternatively spliced form of the human CD94 gene.";

RL Immunogenetics 47:305-309(1998).

RN [5] SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Blood;

RX MEDLINE=22388257; PubMed=124477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schulter G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhattacharya R., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soresi M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Villalon D.K., Mizany D.M., Sodergren B.J., Lu X., Gibbs R.A., PA Whiting M., Madan A., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smailus D.E., Schnarch A., Schein J.B., Jones S.J.M., Marra M.A., PA RT human and mouse cDNA sequences.";

RA RT generation and initial analysis of more than 15,000 full-length RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16839-16903 (2002).

CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-B molecules by NK cells and some cytotoxic T-cells.

CC -!- SUBUNIT: Can form disulfide-linked heterodimer with NGK2 family members.

CC -!- SUBCELLULAR LOCATION: Type II membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=3;

CC CC Name=1; Synonyms=CD94-A; IsoID=Q13241-1; Sequence=Displayed;

CC CC Name=2; Synonyms=CD94-B; IsoID=Q13241-2; Sequence=VSP\_003053;

CC CC Name=3; Synonyms=CD94 alt; IsoID=Q13241-3; Sequence=VSP\_003052;

CC -!- TISSUE\_SPECIFICITY: Natural killer cells

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

CC -!- DATABASE: NAME=PROW; NCBI=9606; guid CD94 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch).

CC CC AAC50291.1;

CC DR EMBL; U10610; AAC50291.1;

CC DR EMBL; Y14287; CAA74663.1; JOINED.

CC DR EMBL; AJ000673; CAA04230.1;

CC DR EMBL; AJ00001; CAA03845.1;

CC DR EMBL; AB009597; BAA2445.1;

CC DR EMBL; AB010084; BAA2445.1;

CC DR EMBL; BC028009; ANH28009.1;

CC DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

CC DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver.); TAS.

CC DR GO; GO:0007166; P:cell surface receptor linked signal transdu.; TAS.

CC DR InterPro; IPR01304; Lectin\_C.

CC DR MTM; 60289;

CC DR GO; GO:0004888; F:transmembrane receptor activity; TAS.

CC DR PROSITE; PS00615; C\_TYPELECTIN\_1; FALSE\_NEG.

CC DR PROSITE; PS00041; C\_TYPELECTIN\_2; 1.

CC KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; 3D-structure.

CC FT DOMAIN 1 10 CTOPLASMIC (POTENTIAL).

CC FT DOMAIN 11 31 SIGNAL\_ANCHOR (TYPE-II MEMBRANE PROTEIN)

CC FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).

CC FT DISULFID 61 72 BY SIMILARITY.

CC FT DISULFID 89 174 BY SIMILARITY.

CC FT DISULFID 152 166 BY SIMILARITY.

CC FT CARBOHYD 83 132 N-LINKED (GLCNAC- . ) (POTENTIAL).

CC FT CARBOHYD 132 132 N-LINKED (GLCNAC- . ) (POTENTIAL).

CC FT VARSPlic 1 34 MAVFKTYWLISGTLGICHSLMATTGILLKNS -> MAA (in isoform 3).

CC FT VARSPlic 105 105 /FTId=VSP\_003052.

CC SQ SEQUENCE 179 AA; 20497 MW; 188499EP003053;

CC Query Match 19.2%; Score 196.5; DB 1; Length 179;

CC Best Local Similarity 32.7%; Pred. No. 8.6e-12;

CC Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

CC OY 35 CSCIVATIGIUTAVILSUYWILQGSN -YSCTACSPCSCPDBMKYGNHCFYFSVE 92

CC 20 CLSLMA-TLGILKNSPTKLSTEPAFTPGPNTLEQDSDCSSCQERVGTRNCNYCTTSE 78

CC 93 EKDWNSSLEFLCLARDHLLVLTNDQNSLLQFLSAPFCWTGL --RNNNSWRWEQSPL 149

CC 79 QKTNWNEHRHLCSQSKQLQNTEDFMS -SSQFYWGLSVEEHTAWLWNGSAL 136

CC 150 NFSRISSNSF ---YOTGCAINKN-LQASSEVPLHGVCCK 186

CC 137 -SQYLPFSFETNTKCIATNPNGLADESCKNRYICK 176



|  |   |  |
|--|---|--|
| DR   | EMBL; AF259054; AAF86964.1; -.  | -!- SIMILARITY: Contains 1 C-type lectin family domain.  |
| DR   | HSSP; P22877; IEGG.   | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch). |
| DR   | Pfam; PF0059; Lectin_C.   | CC   |
| DR   | InterPro; IPR001304; Lectin_C.  | CC   |
| DR   | SMART; SM00034; CLECT; 1.   | CC   |
| DR   | PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.   | CC   |
| DR   | PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   | CC   |
| KW   | Alternative; Receptor; Glycoprotein; Transmembrane; signal-anchor; Lectin;  | CC   |
| KW   | Alternative splicing  | CC   |
| FT   | DOMAIN 1 10   | CC   |
| FT   | TRANSMEM 11 31  | CC   |
| FT   | CYTOSPLASMIC (POTENTIAL).   | CC   |
| FT   | SIGNAL_ANCHOR (TYPE-III MEMBRANE PROTEIN)   | CC   |
| FT   | (POTENTIAL).  | CC   |
| FT   | EXTRACELLULAR (POTENTIAL).  | CC   |
| FT   | C-TYPE LECTIN (LONG FORM).  | CC   |
| FT   | BY SIMILARITY.  | CC   |
| FT   | DISULFID 89 174   | DR MGI:107540; Klrbla.   |
| FT   | DISULFID 152 166  | DR InterPro; IPR002353; AntifreezeII.  |
| FT   | CARBODY 83 83   | DR InterPro; IPR001304; Lectin_C.  |
| FT   | CARBODY 132 132   | DR Pfam; PF00059; lectin_c_1.  |
| FT   | VARSPLIC 105 105  | DR PRINTS; PR00356; ANTIFREEZEII.  |
| FT   | L -> LQ (in isoform 2).   | DR SMART; SM00034; CLCET_1.  |
| FT   | /ETID:VSP /PS003056.  | DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.   |
| SQ   | SEQUENCE 179 AA; 20493 MW; 7244D97ED9587E7 CRC64;   | DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   |
| Query Match  | Score 194.5; DB 1; Length 179;  | KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  |
| Best Local Similarity  | 19.0%; Pred. No. 1..3e-11;  | FT FT  |
| Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7; | FT FT   | FT FT  |
| QY   | 35 CSCNVAITLGHLTAVILSLLYQWLICQSN--YKTCASCPSCPDRWMKGHNHCYVFSTV 92  | FT FT  |
| Db   | 20 CLSMA-TGLGKLKNSTKLISPAFTGPNTIELQKDSDOCSCQEKWGYCRNCYFISSE 78  | FT FT  |
| QY   | 93 EKDWNSSLERFLDARDSHLAVTDNQEMSLQVELSEAFFCMGL--RANNSGWRWEDGSPL 149  | FT FT  |
| Db   | 79 QKTWTNESRHLCAQSSESSLLOLQNTDELDMS -SSQQFWIGLSSYSEETHAWLWENGSSAL 136   | FT FT  |
| QY   | 150 NFSRISNSF---VQTGCAINKNG-LOASSCEVPLHGYCKK 186  | FT FT  |
| Db   | 137 --SQYLFPSPETFNPKNCIAYNPNGNALDESCDKRYCKQ 176   | FT FT  |
| Query Match  | Score 191; DB 1; Length 227;  | FT FT  |
| Best Local Similarity  | 18.7%; Pred. No. 3.8e-11;   | FT FT  |
| Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7; | FT FT   | FT FT  |
| QY   | 24 PQQKSSSSRPSCSCLVATUGLL-TAVLLSVLYQ-----WLGQS-NYST-OASCP 74  | FT FT  |
| Db   | 34 PRSHRSALKLSCAGHILLVVTLLGMSVLVRVLIQKPSLEKCYVLLQENLNKTTDSAKL 93  | FT FT  |
| QY   | 75 CPDWMKTYGNHCYFYSVEWKDNMSSLEFLARDSHLTVTDNQEMSLQVELSEA-F-CW 132  | FT FT  |
| Db   | 94 CPQDWLSHEDXKCFFIVSQVSNTWEGLVDDGKATMLIQDQEFLRFLDSIKEKYNSFW 153  | FT FT  |
| QY   | 133 IGHR--NNSGFWEDGSPLNFS -RISNSFVQTCGAINKGQLASSCEVPLHGCK 186   | DE DE  |
| Db   | 154 IGLRTLPDMWNKWTNGSTLNSDVLKITGDENDSCAAISGDKRVTFESCNSDNRWICQR 212  | DE DE  |
| RESULT 7   | NKG2A HUMAN STANDARD; PRT; 227 AA.  | DE DE  |
| NKG2_MOUSE   | STANDARD; PRT; 227 AA.  | DE DE  |
| ID   | NKG2A HUMAN STANDARD; PRT; 227 AA.  | GN NK cell receptor A.   |
| AC   | P2715;  | GN KIR1 OR NKG2A.  |
| DT   | 01-AUG-1992 (Rel. 23, Created)  | DT 01-AUG-1992 (Rel. 23, Created)  |
| DT   | 01-AUG-1992 (Rel. 23, Last sequence update)   | DT 01-AUG-1992 (Rel. 23, Last sequence update)   |
| DT   | 28-FEB-2003 (Rel. 41, Last annotation update)   | DT 10-OCT-2003 (Rel. 42, Last annotation update)   |
| DE   | Natural killer cell surface protein PI-2 (NKR-PI_2).  | DE NKG2-B type II integral membrane protein (NKG2-A/B activating   |
| OS   | KIRB1A OR LY55A OR LY55.  | OS Mammalia; Eutheria; Primates; Catarrhini; Homino.   |
| OC   | Mus musculus (Mouse)  | OC Homo sapiens (Human).   |
| OC   | Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;   | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| NCBI_TaxID=10090;  | NCBI_TaxID=9606;  | NCBI_TaxID=9606;   |
| RN   | SEQUENCE FROM N.A. MEDLINE=91349596; PubMed=1800421;  | RN [1]   |
| RX   | Giorla R., Trucco M.; "Mouse NKR-PI, A family of genes selectively coexpressed in adherent lymphokine-activated killer cells."; J. Immunol. 147:1701-1708 (1991). | RX SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).  |
| RX   | [2]   | RX MEDLINE=91178434; PubMed=2007850;   |
| RP   | SEQUENCE FROM N.A. MEDLINE=92013158; PubMed=1680927;  | RX Houchins J.P., Yabe T., McSherry C., Bach F.H.;   |
| RA   | Seaman W.E.; "cDNA cloning of mouse NKR-P1 and genetic linkage with Ly-49."; J. Immunol. 147:3229-3236 (1991).  | RT "DNA sequence analysis of NKG2, a family of related cDNA clones   |
| CC   | -!- FUNCTION: May function as signal-transmitting receptor.   | CC   |
| CC   | -!- SUBUNIT: Homodimer; disulfide-linked.   | CC   |
| CC   | -!- SUBCELLULAR LOCALIZATION: Type II membrane protein.   | CC   |
| CC   | -!- TISSUE SPECIFICITY: Natural killer cells.   | CC   |

RT encoding type II integral membrane proteins on human natural killer cells";  
 RT J. Exp. Med. 173:1017-1020 (1991).  
 RT [2] SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).  
 RPRP MEDLINE:96337918; PubMed=8753859;  
 RPRP Plougastel B., Jones T., Trowsdale J.;  
 RPRP "Genomic structure, chromosome location, and alternative splicing of the human NKG2A gene.";  
 RPRP Immunogenetics 44:286-291 (1996).  
 RPRP [3] SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).  
 RPRP MEDLINE:98266668; PubMed=9598306;  
 RPRP Plougastel B., Trowsdale J.;  
 RPRP "Sequence analysis of a 62-kb region overlapping the human KLRC cluster of genes.";  
 RPRP Genomics 49:193-199 (1998).  
 RPRP [4] SEQUENCE FROM N.A. (ISOFORMS NKG2-A AND NKG2-B).  
 RPRP MEDLINE:3100257; PubMed=12477932;  
 RPRP Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RPRP Klausner R.D., Collins F.S., Wagner L., Schuler G.D.,  
 RPRP Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.E., Bhat N.K.,  
 RPRP Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RPRP Diatchenko L., Matsunaga K., Farmer A.R., Rubin G.M., Hong L.,  
 RPRP Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RPRP Brownstein M.J., Ustün T.B., Toshiyuki S., Carninci P., Prange C.,  
 RPRP Raha S., Loqueland N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RPRP Bosq S.A., McEwan P.J., Peterman K.J., Malek J.A., Gunaratne P.H.,  
 RPRP Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RPRP Villalon D.K., Murry D.M., Soderquist R.E.J., Lu X., Gibbs R.A.,  
 RPRP Fahay J., Heitton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RPRP Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,  
 RPRP Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RPRP Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RPRP Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
 RPRP Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RPRP "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RPRP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RPRP !- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  
 RPRP !- SUBUNIT: Can form disulfide-bonded heterodimer with CB94.  
 RPRP !- SUBCELLULAR LOCATION: Type II membrane protein.  
 RPRP !- ALTERNATIVE PRODUCTS:  
 RPRP Event-Alternative splicing; Named isoforms=2;  
 RPRP Name=NKG2A;  
 RPRP IsoId=P26715-1; Sequence=Displayed;  
 RPRP Name=NKG2-B;  
 RPRP IsoId=P26715-2; Sequence=VSP 003062;  
 RPRP !- TISSUE SPECIFICITY: Natural killer cells.  
 RPRP !- SIMILARITY: Contains 1 C-type lectin family domain.  
 RPRP  
 RPRP This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation of the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and/or for commercial entities requires a license agreement (See <http://www.isb-sib.ch> or send an email to license@isb-sib.ch).  
 RPRP  
 RPRP EMBL: X54967; CAA38549 1; -;  
 RPRP EMBL: X54858; CAA38650 1; -;  
 RPRP EMBL: U54186; AAB17133 1; -;  
 RPRP EMBL: U54183; AAB17133 1; JOINED;  
 RPRP EMBL: U54184; AAB17133 1; JOINED.

|            |   |  |
|------------|---|--|
| RA         | Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L., Parham P.,   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.   |
| RT         | "Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans."   | NCB_ TaxID=9676; OC RN [1]   |
| RL         | Immunity 12:687-698 (2000).   | SEQUENCE FROM N.A. RX  |
| CC         | -- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  | MEDLINE=9117834; PubMed=2007850; RA  |
| CC         | -- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.  | Houchins J.P., Yabe T., McSherry C., Bach F.H.; RT   |
| CC         | -- SUBCELLULAR LOCATION: Type II membrane protein.  | "DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II integral membrane proteins on human natural killer cells." RT   |
| CC         | -- TISSUE SPECIFICITY: Natural killer cells.  | J. Exp. Med. 173:1017-1020(1991). RT   |
| CC         | -- SIMILARITY: Contains 1 C-type lectin family domain.  | [2]  |
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| CC         | EMBL; APZ59057; AAP86967.1; -;  | RP SEQUENCE FROM N.A. RX   |
| CC         | EMBL; AF259059; AAP86969.1; -;  | RC TISSUE=Lymphoid; RA Biassoni R.;  |
| CC         | EMBL; APZ59060; AAP86970.2; -;  | PL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. RN [4]   |
| CC         | HSSP; PD5451; LLTR.   | RP SEQUENCE FROM N.A. AND VARIANTS ASN-2 AND PHE-102. RX   |
| CC         | InterPro; IPR001304; Lectin_C.  | MEDLINE=2162389; PubMed=11751968; RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.; RT "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex," RL Immunogenetics 48:163-173 (1998). RT NKG2 Genes." RL Immunol. 168:240-252(2002).  |
| CC         | Pfam; PF00059; lectrin_C_1.   | CC -1- PROJECTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. CC -1- SUBUNIT: Can form disulfide-bonded heterodimer with CD94. CC -1- SUBCELLULAR LOCATION: Type II membrane protein. CC -1- TISSUE SPECIFICITY: Natural killer cells. CC -1- SIMILARITY: Contains 1 C-type lectin family domain.   |
| CC         | SMART; SM00034; CBCT; 1.  | CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch). |
| CC         | PROSITE; PS50041; C-TYPE LECTIN_2; 1.   | CC DR EMBL; AJ001664; CAA04922.1; -. DR EMBL; Y13055; CAA73498.1; -. DR EMBL; AF260134; AA86572.1; -. DR PIR; PT0374; PT0374.  |
| CC         | KW Receptor; Transmembrane; Multigene family; signal-anchor; Lectin; Glycoprotein.  | DR MIM: 602891; -. DR GO; GO:0005887; C:integral to plasma membrane; TAS. DR GO; GO:0004888; F:transmembrane receptor activity; TAS. DR GO; GO:0006568; P:cellular defense response; TAS. DR InterPro; IPR01304; Lectin_C. DR Pfam; PF00059; Lectin_C. DR SMART; SM00034; CLBC_1. DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG. DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.  |
| CC         | FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).   | KW Receptor; Transmembrane; Multigene family; signal-anchor; Lectin; Glycoprotein; Polymorphism. FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).   |
| CC         | FT TRANSMEM 1 71 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)   | FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)   |
| FT         | DR DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).   | FT DOMAIN 94 231 EXTRACELLULAR (POTENTIAL).  |
| FT         | DR DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).  | FT DOMAIN 116 229 C-TYPE LECTIN (LONG FORM).   |
| FT         | DR DISULFID 117 128 BY SIMILARITY.  | FT DOMAIN 117 128 BY SIMILARITY.   |
| FT         | DR DISULFID 145 227 BY SIMILARITY.  | FT DOMAIN 145 227 BY SIMILARITY.   |
| FT         | DR DISULFID 206 219 BY SIMILARITY.  | FT DOMAIN 206 219 BY SIMILARITY.   |
| FT         | DR CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).   | FT DOMAIN 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT         | DR CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).   | FT DOMAIN 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT         | DR VARIANT 60 60 N-> D (in allele NKG2-C*101).  | FT VARIANT 60 60 N-> D (in allele NKG2-C*101).   |
| FT         | DR VARIANT 232 233 Missing (in allele NKG2-C*103).  | FT VARIANT 232 233 Missing (in allele NKG2-C*103).   |
| FT         | DR SEQUENCE 233 AA; 26169 MW; 18C04D1B91E1B7CA CRC64;   | FT SEQUENCE 233 AA; 26169 MW; 18C04D1B91E1B7CA CRC64;  |
| FT         | Query Match 18.3%; Score 187; DB 1; Length 233;   | FT Best_local_Similarity 28.4%; Pred. No. 9.4e-11; Indels 30; Mismatches 48; Conservative 30; Gaps 5;  |
| FT         | Matches 48; Consecutive 30; Mismatches 77; Indels 14; Gaps 5;   | FT DR EMBL; X54869; CAA38651.1; -. DR EMBL; AJ001664; CAA04922.1; -. DR EMBL; Y13055; CAA73498.1; -. DR EMBL; AF260134; AA86572.1; -. DR PIR; PT0374; PT0374.  |
| QY         | 24 PQKQSSSSRPSCSCLVAVATLGILPAVLLVLYWILCGNSVYST---CASCPSCPDRW 79   | FT DR GeneWise: HGNC-6375; KLRC2.  |
| Db         | 67 PPEKLTAEVIGLICCVV----LMATVLKIVLIPPLEQNNSNTGTQKARHGHCHCPDEW 121   | FT DR MIM: 602891; -. DR GO; GO:0005887; C:integral to plasma membrane; TAS. DR GO; GO:0004888; F:transmembrane receptor activity; TAS. DR GO; GO:0006568; P:cellular defense response; TAS. DR InterPro; IPR01304; Lectin_C. DR Pfam; PF00059; Lectin_C. DR SMART; SM00034; CLBC_1. DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.  |
| QY         | 80 MKYGNHCTYFSVEEKDWNSLLEFLCLARDHLLVITDNOEMSLLQVFLSEAFCWIGL-RNN 138   | KW Receptor; Transmembrane; Multigene family; signal-anchor; Lectin; Glycoprotein; Polymorphism. FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).   |
| Db         | 122 ITIVNSNCTYIGKERRTWEBSLLACTSKNSGGLS1DNEEMKFELATISPS--WIGVFNNS 179  | FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).  |
| QY         | 139 SIGWWEDGGPLNFSR--ISSLNSFVQTGCKINKGLQASSCEVLHGCK 185   | FT DOMAIN 116 229 EXTRACELLULAR (POTENTIAL).   |
| Db         | 180 SHHPWVTINGLAFKHEIIIDSDAELNCAVQVKGLKSACGSSSTIYHCK 228  | FT DOMAIN 117 128 BY SIMILARITY.   |
| OS         | RESULT 9  | FT DOMAIN 145 227 BY SIMILARITY.   |
| NKG2_HUMAN | ID P26717; O43802; QNR42; STANDARD; PRT; 231 AA.  | FT DOMAIN 145 227 BY SIMILARITY.   |
| AC         | 01-AUG-1992 (Rel. 23, Created)  | FT DOMAIN 145 227 BY SIMILARITY.   |
| DT         | 28-FEB-2003 (Rel. 41, Last sequence update)   | FT DOMAIN 145 227 BY SIMILARITY.   |
| DT         | 28-FEB-2003 (Rel. 41, Last annotation update)   | FT DOMAIN 145 227 BY SIMILARITY.   |
| DE         | NKG2-C type II integral membrane protein (NKG2-C activating NK receptor) (NK cell receptor C).  | FT DOMAIN 145 227 BY SIMILARITY.   |
| DE         | KURC2 OR NKG2C.   | FT DOMAIN 206 219 BY SIMILARITY.   |
| OS         | Homo sapiens (Human).   |  |

FT CARBOYD 100 100 N-LINKED (GLCNAC, . ) (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT CARBOYD 149 149 N-LINKED (GLCNAC, . ) (POTENTIAL). (POTENTIAL).  
 FT CARBOYD 178 178 N-LINKED (GLCNAC, . ) (POTENTIAL). EXTRACELLULAR (POTENTIAL).  
 FT VARIANT 2 2 S -> N (in allele NKG2-C\*02). C-TYPE LECTIN (LONG FORM).  
 /FTId=VAR 013404.  
 FT VARIANT 102 102 S -> P (in allele NKG2-C\*02). BY SIMILARITY.  
 /FTId=VAR 013405.  
 FT CONFLICT 161 161 M -> I (IN REF. 1). BY SIMILARITY.  
 SEQUENCE 231 AA; 26072 MW; 6B971EECD7542330 CRC64; N-LINKED (GLCNAC, . ) (POTENTIAL).  
 Query Match 18.2%; Score 186; DB 1; Length 231; N-LINKED (GLCNAC, . ) (POTENTIAL).  
 Best Local Similarity 28.4%; Pred. No. 1\_2e-10; N-LINKED (GLCNAC, . ) (POTENTIAL).  
 Matches 48; Conservative 31; Mismatches 76; Indels 14; Gaps 5; SQ SEQUENCE 216 AA; 25075 MW; A44833F3140DEAC CRC64;  
 Query Match 17.9%; Score 183.5; DB 1; Length 216;  
 Best Local Similarity 26.2%; Pred. No. 1.9e-10;  
 Matches 49; Conservative 40; Mismatches 75; Indels 23; Gaps 6;  
 /FTId=VAR 013404.  
 Db 67 EPEKLTPEVLGLICIV----LMATVKTIVLIPFLQINNSSPNTTKQAHCGHCEEW 121  
 Qy 80 MKYGNHCCYYFSVEKDQNSLLEFLCLADSLLVITDNOEMSLLQVFLSEAFCWIGL-RNN 138  
 Db 122 ITYNSNCYYIGERRTWEESSLACTSSNSLISDNEMEKKELASLPS--WIGYFRNS 179  
 Qy 139 SGWRDGGSPNFSR--ISSNSPVQTGAINNGLOSSPESVPLHGCK 185  
 Db 180 SHHPWVTINGLAFKHKIKDSDNAELNCAVLQVNRLKSAQCQSSMIXCK 228  
 RESULT 10  
 NRGD MACMU STANDARD; PRT; 216 AA.  
 ID NKG2 MACMU STANDARD; PRT; 233 AA.  
 AC Q9MZJ7; Q9MZJ8; Q9MZJ9; Q9MZJ1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE NKG2-D type II integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).  
 GN Macaca mulatta (Rhesus macaque).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A. MEDLINE=20322487; PubMed=10866118;  
 RA LaBonte M.L., Levy D.B., Letvin N.L.;  
 RT "Characterization of rhesus monkey CD94/NKG2 family members and  
 identification of novel transmembrane-deleted forms of NKG2-A, B, C,  
 and D";  
 RL Immunogenetics 51:496-499 (2000).  
 CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  
 CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -I- TISSUE SPECIFICITY: Natural killer cells.  
 CC -I- SIMILARITY: Contains 1 C-type lectin family domain.  
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 CC ---  
 CC DR EMBL; AP190943; AAP74539.1; -;  
 CC DR InterPro; IPB001304; Lectin\_C;  
 CC DR Pfam; PF00059; Lectin\_c; 1.  
 CC SMART; SM00044; CNECT; 1.  
 CC DR PROSITE; PS50041; C\_TYPELECTIN\_2;  
 KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;  
 KW Glycoprotein; Polymorphism.  
 KW DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).  
 FT

FT TRANSMEM 52 72  
 FT DOMAIN 73 216  
 FT DOMAIN 98 213  
 FT DOMAIN 99 210  
 FT DISULFID 127 211  
 FT DISULFID 189 203  
 FT DISULFID 189 203  
 FT CARBOYD 115 115  
 FT CARBOYD 131 131  
 FT CARBOYD 163 163  
 FT CARBOYD 202 202  
 SQ SEQUENCE 216 AA; 25075 MW; A44833F3140DEAC CRC64;  
 Query Match 17.9%; Score 183.5; DB 1; Length 216;  
 Best Local Similarity 26.2%; Pred. No. 1.9e-10;  
 Matches 49; Conservative 40; Mismatches 75; Indels 23; Gaps 6;  
 /FTId=VAR 013404.  
 Qy 15 ATQAQNDYGPQRS---SSSKPSCSCLVAITLG-----LTAVLSSVLQYQWLICQ 62  
 Db 31 STRCQRORCPYTKCRENASLFFCCPIAYAMGIRFLIMTIWSAVFLNSIFNQEIQIP 90  
 Qy 63 GSNSYSTACASCPCPDWMMKYGHCTYSVEKDKDWNNSLEFLCLARDSHLLVITDNOQMSLL 122  
 Db 91 --LTESYCGHPPKWCYKNQNCFYOFNESKNWTSQASCMSQNSSLKTYSKEDDLL 146  
 Qy 123 QYVFLSEAFCWIGL---RNNSGWRWEDGSPLNSRRISSNSFVQTGAINKG1Q-A--SSCE 177  
 Db 147 K--LVTSYHWWGILVHLPTGNSQWEDGSILSPNLLTIEMOKGDCALYASSFKGYTENCS 204  
 RESULT 11  
 NKG2 MACMU STANDARD; PRT; 233 AA.  
 ID NKG2 MACMU STANDARD; PRT; 233 AA.  
 AC Q9MZJ3; Q9MZJ8; Q9MZJ9; Q9MZJ1;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE NKG2-A/NKG2-B type II integral membrane protein (NKG2-A/B activating NK receptor) (NK cell receptor A).  
 GN NKG2A.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Birkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butheria; Primates; Catarrhini; Cercopithecoidea.  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS NKG2-A; NKG2-B AND NKG2-BDTM).  
 RX MEDLINE=20322487; PubMed=10866118;  
 RA LaBonte M.L., Levy D.B., Letvin N.L.;  
 RT "Characterisation of rhesus monkey CD94/NKG2 family members and  
 identification of novel transmembrane-deleted forms of NKG2-A, B, C,  
 and D";  
 RL Immunogenetics 51:496-499 (2000).  
 CC -I- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  
 CC -I- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.  
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -I- IDENTIFICATION: Identification of novel transmembrane-deleted forms of NKG2-A, B, C,  
 CC and D.";  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=NKG2-A;  
 CC IsoId=Q9MZJ3-1; Sequence=Displayed;  
 CC Name=NKG2-B;  
 CC IsoId=Q9MZJ3-2; Sequence=VSP\_003064;  
 CC Name=NKG2-Adm;  
 CC IsoId=Q9MZJ3-3; Sequence=VSP\_003063;  
 CC Name=NKG2-Bdtm;  
 CC IsoId=Q9MZJ3-4; Sequence=VSP\_003065;  
 CC ---  
 CC -I- TISSUE SPECIFICITY: Natural killer cells.  
 CC -I- SIMILARITY: Contains 1 C-type lectin family domain.

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|   |    |  |                |
|---|----|--|----------------|
| CC  | OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |                |
| CC  | OC | NCBI_TAXID=9606;   |                |
| CC  | RN | SEQUENCE FROM N.A.   |                |
| CC  | RP | SEQUENCE FROM N.A.   |                |
| CC  | RX | Medline=91178434; PubMed=2007850;  |                |
| CC  | RA | Houchins J.P., Yabe T., McSherry C., Bach F.H.;  |                |
| CC  | RT | "DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II integral membrane proteins on human natural killer cells.";   |                |
| CC  | RT | J. Exp. Med. 173:1017-1020 (1991).   |                |
| DR  | RL | SEQUENCE FROM N.A.   |                |
| EMBL; AF190979; AFAF73835; 1;   | RN | Medline=98350122; PubMed=9683661;  |                |
| EMBL; AF190981; AFAF73837; 1;   | RA | Gilenke J., Sobanov Y., Brostjan C., Steffens C., Nguyen C., Lehrach H., Hofer E., Francis F.;   |                |
| EMBL; AF190982; AFAF73838; 1;   | RA | "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex,";   |                |
| EMBL; AF190984; AFAT73840; 1;   | RL | Immunogenetics 48:163-173 (1998).  |                |
| DR  | RN | SEQUENCE FROM N.A.   |                |
| P22897; LEGG; InterPro; IPR001304; Lectin_C; PTm; PR00059; lectin_c; C;   | RA | Kothapalli R., Kusmartseva I., Loughran T.P. Jr.;  |                |
| SMART; SM00034; CLECT; 1;   | RX | "Identification and characterization of the NKG2D gene from large granular lymphocytic leukemia (LGL) cells";  |                |
| PROSITE; PS00615; C_TYPELECTIN_1; FALSE_NEG.  | RA | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  |                |
| PROSITE; PS00615; C_TYPELECTIN_2; 1;  | RT | [2]  |                |
| DR  | RT | SEQUENCE FROM N.A. AND VARIANT THR-72.   |                |
| PROSITE; PS50041; C_TYPELECTIN_2; 1;  | RX | Medline=21623889; PubMed=11751968;   |                |
| Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; KW  | RA | Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Clelland S., Guethlein L.A., Uhrberg M., Parham P.;   |                |
| Glycoprotein; Alternative Splicing; DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).  | RA | "Conservation and variation in human and common chimpanzee CD94 and NKG2 genes";   |                |
| FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).   | RT | RT   |                |
| FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).   | RL | RT   |                |
| FT DOMAIN 118 231 C-TYPE LECTIN (LONG FORM).  | RN | RT   |                |
| FT DISULFID 119 130 BY SIMILARITY.  | RP | RT   |                |
| FT DISULFID 147 229 BY SIMILARITY.  | RX | RT   |                |
| FT FT 208 221 BY SIMILARITY.  | RA | SEQUENCE FROM N.A.   |                |
| FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).   | RA | RT   |                |
| FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).   | RA | RT   |                |
| FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).   | RA | RT   |                |
| FT VARSPLIC 63 95 DISLAREKVLNGHLIGLICVILMASVTVWVIPS -> A (in isoform NKG2-Act_m).   | RA | RT   |                |
| FT VARSPLIC 96 113 Missing (in isoform NKG2-B).   | RN | RT   |                |
| FT VARSPLIC 63 112 Missing (in isoform NKG2-Bdtm).  | RC | TISSUE=Testis;   |                |
| FT VARSPLIC 63 112 /FTid=VSP 003063.  | RX | Medline=2238257; PubMed=12477932;  |                |
| SQ SEQUENCE 233 AA; 26286 MW; 237B2B536B489E76 CRC64;   | RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Collins F.S., Wagner L., Shemesh C.M., Schaefer C.F., Bhat N.K., Hopkins R.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong S.W., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Rataj S.S., Logueilano N.A., Peters G.J., McKernan R.D., Mullally S.J., Bosq S.A., McEwan P.J., Worley K.C., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia L.J., Hulyk S.W., Villalon D.K., Mozny D.M., Sodegran E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez R.W., Touchman J.W., Green P.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J.J., Myers R.M., Scherich A., Schein J.E., Jones J.M., Marrs M.A., Schnurch A., Skalska U., Smilus D.E., RT | TISSUE=Testis; |
| Matches 52; Conservative 34; Mismatches 81; Indels 22; Gaps 7; Score 17.9%; Best Local Similarity 21.5%; Pred. No. 2.3e-10; | RA | "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  |                |
| QY 5 VIVSMLETTATQAOQDYGPQQKSSSSKSCSC--LYVLTGILTAVL---SVLVQ 57   | RA | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).   |                |
| Db 38 ITYVABLNQTKTSQ--DFFQNDKTNHCQKULLSAPEKLQAGLGLICVLMASVTVWVIPS 94  | RA | -1- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  |                |
| Qy 58 WLLCGGSNTS-----CASCPSCPDRMKYCNHCVYFSVEEKDWNSLEFLCLARDSH 110   | RT | -1- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.  |                |
| Db 95 STLTQHNNSLNLTRTQKARHCHGCPENITYNSCYTICKERWTAAELACTSKNSL 154  | CC | -1- SUBCELLULAR LOCATION: Type II membrane protein.  |                |
| Qy 111 LVTTDNQENSLLQVLFSEAFCWIGL-RNNSGWREDGSPLNFSR-ISSNSFYQTGAIN 167  | CC | -1- TISSUE SPECIFICITY: Natural killer cells.  |                |
| Db 155 LSIDNEEEFKLTALLS--WIDVFRDSSHHPWVTINGLTFRHBKEEDHABHNCAMH 212  | CC | CC   |                |
| Qy 168 KNGLQASSC 176  | CC | CC   |                |
| Db 213 VRGLFSDDEC 221   | CC | CC   |                |
| RESULT 1.2  | CC | CC   |                |
| NKG2D_HUMAN   | CC | CC   |                |
| ID NKG2D_HUMAN STANDARD; PRT; 216 AA.   | CC | CC   |                |
| AC P26718; Q9NR41; 01-AUG-1992 (Rel. 23, Created)   | CC | CC   |                |
| DT 01-AUG-1992 (Rel. 23, Last sequence update)  | CC | CC   |                |
| DT 10-OCT-2003 (Rel. 42, Last annotation update)  | CC | CC   |                |
| DE NKG2-D type II integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).                           | CC | CC   |                |
| DN NKG2D.   | CC | CC   |                |
| OS Homo sapiens (Human).  | DR | EMBL; X54870; CAA38652.1; -  |                |

|   |   |  |
|---|---|--|
| DR  | EMBL; AJ001687; CAA04925.1; -.  | "Natural killer lectin-like receptors have divergent carboxy-terminal, distinct from C-type lectins."  |
| DR  | EMBL; AJ001688; CAA04925.1; JOINED.   |  |
| DR  | EMBL; AJ001689; CAA04925.1; -.  |  |
| DR  | EMBL; AF461811; AAL6523.1; -.   |  |
| DR  | EMBL; AF260135; AAF86973.1; -.  |  |
| DR  | EMBL; AF260136; AAF86974.1; -.  |  |
| DR  | EMBL; BC039836; AAH39836.1; -.  |  |
| DR  | PIR; PT0375; PT0375.  | "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex."  |
| DR  | PDB; 1HYR; 23-MAY-01.   |  |
| DR  | PDB; 1KCG; 09-JAN-02.   |  |
| DR  | GO; GO:0005987; C:integral to plasma membrane; TAS.   |  |
| DR  | GO; GO:0004872; F:receptor activity; TAS.   |  |
| DR  | GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . . ; TAS.   |  |
| DR  | InterPro; IPR002353; Antifreezell.  |  |
| DR  | InterPro; IPR001304; Lectin_C.  |  |
| DR  | PRINTS; PR00359; Lectin_c_1.  |  |
| DR  | PRINTS; PR00356; ANTIFREEZILL.  |  |
| DR  | SMART; SM00034; CLECT_1.  |  |
| DR  | PROSITE; PS50041; C_TYPE_LECTIN_1; FALSE_NEG.   |  |
| DR  | KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;  |  |
| DR  | Glycoprotein; Polymorphism; 3D-structure.   |  |
| FT  | DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).  |  |
| FT  | TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  | "Conservation and variation in human and common chimpanzee CD94 and NKG2 genes."   |
| FT  | DOMAIN 73 216 EXTRACELLULAR (POTENTIAL).  |  |
| FT  | DOMAIN 98 213 C-TYPE LECTIN (LONG FORM).  |  |
| FT  | DISULFID 99 110 BY SIMILARITY.  |  |
| FT  | DISULFID 127 211 BY SIMILARITY.   |  |
| FT  | DISULFID 189 203 BY SIMILARITY.   |  |
| FT  | CARBONYD 131 131 N-LINKED (GLCNAC . . . ) (POTENTIAL).  |  |
| FT  | CARBONYD 163 163 N-LINKED (GLCNAC . . . ) (POTENTIAL).  |  |
| FT  | CARBOYD 202 202 N-LINKED (GLCNAC . . . ) (POTENTIAL).   |  |
| FT  | VARIANT 72 72 A -> T (in allele NKG2-D*02).   |  |
| FT  |   | /FTID=VAR 013295   |
| SQ  | SEQUENCE 216 AA; 25274 MW; C22FBBD533D780B CRC64; Query Match 17.6%; Score 180; DB 1; Length 216; Best Local Similarity 26.8%; Pred. No. 4e-10; Matches 42; Conservative 31; Mismatches 52; Gaps 5; Matches 42; Conservation 31; Mismatches 52; Gaps 5; |  |
| Qy  | 37 CLVAAITG-----LITAVILSVLQLQWLQCGSNYSTCASCPSCPDRMKYGNHICYY 88  | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch) |
| Db  | 57 CFIAVAMIRFLIMVAWSQNLNQEVOLP---LTBEYCGPPCKWIVCYQ 112  |  |
| Qy  | 89 PSVVEKDNSSLEPCLARDSHLIVITDQNEMSLQVLFSEAFWIGH--RNNSGMRWED 145   |  |
| Db  | 113 FFDESKNYESQSMQNQASLKVSKEDQDLIK-LVKSYHPIPTNGSWSQWED 170  |  |
| Qy  | 146 GSPLNFSR-----SSNSFVQTCGAIN 167  |  |
| Db  | 171 GSTLSPLNLTLEMQRGDALYASSFFKGYIENCSTPN 207  |  |
| RESULT 13   | NKG2_HUMAN STANDARD; PRT; 240 AA.   |  |
| ID  | NKG2_HUMAN STANDARD; PRT; 240 AA.   |  |
| Q07444; Q96RL0; Q9UP04;   |   |  |
| DT 01-NOV-1997 (Rel. 35, Created)   |   |  |
| DT 01-NOV-1997 (Rel. 35, Last sequence update)  |   |  |
| DT 28-FEB-2003 (Rel. 41, Last annotation update)  |   |  |
| DE NKG2-E type II integral membrane protein (NKG2-E activating NK receptor) (NK cell receptor E).                               |   |  |
| GN KLRC3 OR NKG2E.  |   |  |
| OS Homo sapiens (Human).  |   |  |
| OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Metazoa; Primates; Catarrhini; Hominoidea; Homo. |   |  |
| OX NCBI_TaxID=9606;   |   |  |
| RN [1]  |   |  |
| RP SEQUENCE FROM N.A. (ISOFORM NKG2-E).   |   |  |
| RX MEDLINE=94102823; PubMed=8276468;  |   |  |
| RA Adamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;   |   |  |

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 227 240 RRGFTMLTRIVLNS -> VSISFRKALELAVHQIKFY-CS  
 NRNDMIA (in isoform NKG2-H).  
 FT /FTID=VSP\_03007.  
 FT VARIANT 1.9 19 P -> R (in allele NKG2-B\*02).  
 FT VARIANT 135 135 R -> S (in dbSNP:1138437).  
 FT SEQUENCE 240 AA; 27012 MW; 20591FB21274D8A6 CRC64;  
 Query Match Score 178.5; DB 1; Length 240;  
 Best Local Similarity 28.6%; Pred. No. 6.3e-10;  
 Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;  
 Qy 24 PQQKSSSKPSCSCLVIAITGLLPAVLLSVLYOMILCQGSNYST---CASCPSCPDRW 79  
 Db 67 PPEKLTAEVIGIICIV---LMAATVLKTIVLIPLEQNNSSPNTRQKARPSCHCPCPEW 121  
 Qy 80 MKYGRHHCYVESVEEKDWNSLLEFLARDSHLIVITDN-QEMSLIQVYESSEAFCWIGL-RN 137  
 Db 122 ITYSNSCYTIGKEERTWEEBLQACASKNSSSLSDNEEMKFASILPPS--WIGVFEN 179  
 Qy 138 NSGMRWEDGSPLNTFSR--LSSNSFVQTGAINRGLQASSC 176  
 Db 180 SSHHPWPWTNLAKPKHEITKDSDAERNCAHLHVPGLISDOC 220

## RESULT 14

NKGE\_PANTR ID NKGE\_PANTR STANDARD; PRT; 240 AA.  
 AC O9RM14; O9SM13;  
 DT 29-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE NKG2-E type II integral membrane protein (NKG2-E activating NK receptor) (NK cell receptor E).  
 GN KLRC3 OR NKG2E.  
 OS Pan troglodytes (Chimpanzee).  
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=9598;  
 [1] RP SEQUENCE FROM N.A.' AND VARIANT ARG-213.  
 RX MEDLINE-21621889; PubMed-1151968;  
 RA Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guehlein L.A., Uhrberg M., Parham P.; RT "Conservation and variation in human and common chimpanzee CD94 and NKG2 Genes.";  
 RL J. Immunol. 168:240-252(2002).  
 CC -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  
 CC -!- SUBUNIT: Can form disulide-bonded heterodimer with CR94.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -!- TISSUE SPECIFICITY: Natural killer cells.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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 DR EMBL; AA350006; AAK83793; 1;  
 DR AP350007; AAK83794; 1;  
 DR InterPro; IPR001304; Lectin\_C;  
 DR Pfam; PF00059; lectin\_c; 1;  
 DR SMART; SM0034; CBCT; 1;  
 DR InterPro; IPR01304; Lectin\_C;  
 DR Pfam; PF00059; lectin\_c; 1;  
 DR PRINTS; PR00356; ANTIFREEZII.  
 DR EMBL; M62891; AAA1710.1; -;  
 DR PIR; A35917; A35917;  
 DR HSSP; P22897; 1EGG.  
 DR InterPro; IPR0253; AntifreezeII.  
 DR InterPro; IPR01304; Lectin\_C;  
 DR Pfam; PF00059; lectin\_c; 1;  
 DR PRINTS; PR00356; ANTIFREEZII.

Query Match Score 177.5; DB 1; Length 240;  
 Best Local Similarity 28.0%; Pred. No. 7.9e-10;  
 Matches 45; Conservative 30; Mismatches 71; Indels 15; Gaps 5;  
 Qy 24 PQQKSSSKPSCSCLVIAITGLLPAVLLSVLYOMILCQGSNYST---CASCPSCPDRW 79  
 Db 67 PPEKLTAEVIGIICIV---LMAATVLKTIVLIPLEQNNSSPNTRQKARPSCHCPCPEW 121  
 Qy 80 MKYGRHHCYVESVEEKDWNSLLEFLARDSHLIVITDN-QEMSLIQVYESSEAFCWIGL-RN 138  
 Db 122 ITYSNSCYTIGKEERTWEEBLQACASKNSSSLSDNEEMKFASILPPS--WIGVFEN 179  
 Qy 139 SG--WWRWEDGSPLNTFSR--LSSNSFVQTGAINRGLQASSC 176  
 Db 180 SSHHPWPWTNLAKPKHEITKDSDAERNCAHLHVPGLISDOC 220

RESULT 15

NK1.3 RAT ID NK1.3 RAT STANDARD; PRT; 223 AA.  
 AC P22471; 1;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen DE 3.2.3).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-9037805; PubMed=2399464;  
 RA Giorda R., Rudert W.A., Vavassori C., Chambers W.H., Hiserodt J.C., Trucco M.; RT "NKR-P1, signal transduction molecule on natural killer cells.";  
 RL Science 249:1298-1300(1990).  
 CC -!- FUNCTION: Mediates transmembrane signaling in natural killer (NK) cells and so may act as a receptor able to selectively trigger NK cell activity.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -!- TISSUE SPECIFICITY: Natural killer cells.  
 CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR SMART;SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1;  
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 FT DOMAIN 1 43 CYTOPASMIC (POTENTIAL).  
 FT DOMAIN 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 (POTENTIAL).  
 FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 223 AA; 24551 MW; FCD1B212DDF4330 CRC64;  
 SQ

Query March 17.2%; Score 175.5; DB 1; Length 223;  
 Best Local Similarity 27.1%; Pred. No. 1..le-09;  
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

```

Qy 24 PQQKSSSKPSCSCLVAVTGLI-TAVLLSLLYQ----WILCQQSNYSTCASCPS-- 74
  : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 35 PRSHRLALKLSCAGLILIVLALVGMSLIVRLVQKPSVEPCRVLIQ-ENLSKTGSG-PAKL 92
  : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Qy 75 -CPDRWKYGNHCCYYFSEYKEWNSLEFCLARDSHLLVITDNQEMLLQVF---LSEAFL 130
  | | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 93 KCPKDWLSHRDCKFHVSOTSTIKESLADGGKGATILLVQDQEELFLRNLTKRISSF 152
  ||| | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Qy 131 CWIGLR---NNSGWWRNEDGSPLNFS--RISNSNFVQTGAINTKNGQASSCDEVPLHGVCK 185
  ||| | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 153 -WIGLSYTSLSDENWKWINGSTLNSDVLSITGDETEKDSASVSDKVLSESCLSDNTWVCQ 211
  | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Qy 186 K 186
  | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 212 K 212
  | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |

```

Search completed: August 10, 2004, 16:16:59  
 Job time : 8.35929 secs



XX This is the amino acid sequence of human mast cell function-associated antigen (MAFA), a type II membrane glycoprotein. cDNA (see AAW8198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KUB12 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW8277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternatively spliced forms (see AAW8266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW8258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth.

XX Sequence 189 AA;

|                       |   |                     |            |              |
|-----------------------|---|---------------------|------------|--------------|
| Query Match           | 100.0% ;  | Score 1023 ;        | DB 2 ;     | Length 189 ; |
| Best Local Similarity | 100.0% ;  | Pred. No. 1.8e-98 ; |            |              |
| Matches 189 ;         | Conservative 0 ;  | Mismatches 0 ;      | Indels 0 ; | Gaps 0 ;     |
| Qy                    | 1 MTDSVITYSMLELPATAAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60       |                     |            |              |
| Db                    | 1 MTDSVITYSMLELPATAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60        |                     |            |              |
| Qy                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Db                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Qy                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Db                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Qy                    | 181 HGVCKKYRL 189   |                     |            |              |
| Db                    | 181 HGVCKKYRL 189   |                     |            |              |

RESULT 2  
ID AAE11759 standard; protein; 189 AA.

XX AAE11759;

XX DT 18-DEC-2001 (first entry)

XX Human mast cell function associated antigen (MAFA) protein.

XX Human; pharmaceutical composition; mast cell function associated antigen; KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; KW immunosuppressive; cytostatic.

XX Homo sapiens.

XX WO200170805-A2.

XX PD 27-SEP-2001.

XX PF 16-MAR-2001; 2001WO-US008596.

XX PR 17-MAR-2000; 2000US-0190716P.

XX PA (GEMI-) GEMINI SCI INC.

XX PI Takahashi N, Mikayama T;

XX XX WPI; 2001-611482/70.

XX DR N-PSDB; AAD18734.

XX XX Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

XX PS Claim 10; Page 18; 49pp; English.

CC The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MAFA protein.

|                       |   |                     |            |              |
|-----------------------|---|---------------------|------------|--------------|
| SQ Sequence 189 AA;   | 100.0% ;  | Score 1023 ;        | DB 4 ;     | Length 189 ; |
| Query Match           | 100.0% ;  | Pred. No. 1.8e-98 ; |            |              |
| Best Local Similarity | 100.0% ;  | Mismatches 0 ;      | Indels 0 ; | Gaps 0 ;     |
| Matches 189 ;         | Conservative 0 ;  | Mismatches 0 ;      | Indels 0 ; | Gaps 0 ;     |
| Qy                    | 1 MTDSVITYSMLELPATAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60        |                     |            |              |
| Db                    | 1 MTDSVITYSMLELPATAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60        |                     |            |              |
| Qy                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Db                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Qy                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Db                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |            |              |
| Qy                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Db                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Qy                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Db                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |            |              |
| Qy                    | 181 HGVCKKYRL 189   |                     |            |              |
| Db                    | 181 HGVCKKYRL 189   |                     |            |              |

RESULT 3

ID ADD25635

XX ID ADD25635 standard; protein; 189 AA.

XX AC ADD25635;

XX DT 15-JAN-2004 (first entry)

XX DE Binding domain-immunoglobulin fusion protein; cytosolic;

XX DE antiarthritis; hinge region; immunoglobulin heavy chain;

XX KW neuroprotective; immunosuppressive; antidiabetic; antithyroid;

XX KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;

XX KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;

XX KW rheumatoid arthritis; myasthenia gravis; Grave's disease;

XX KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.

XX OS Unidentified.

XX PN US2003118592-A1.

XX PD 26-JUN-2003.

XX PP 25-JUL-2002; 2002US-00207655.

XX PR 17-JAN-2001; 2001US-067358P.

XX PR 17-JAN-2002; 2002US-0053520P.

XX PR 03-JUN-2002; 2002US-0385691P.

XX PA (GENE-) GENECRAFT INC.

XX XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

|                       |   |                     |              |          |              |
|-----------------------|---|---------------------|--------------|----------|--------------|
| PI                    | Sequence 189 AA;  | 100.0% ;            | Score 1023 ; | DB 4 ;   | Length 189 ; |
| Query Match           | 100.0% ;  | Pred. No. 1.8e-98 ; |              |          |              |
| Best Local Similarity | 100.0% ;  | Mismatches 0 ;      | Indels 0 ;   | Gaps 0 ; |              |
| Matches 189 ;         | Conservative 0 ;  | Mismatches 0 ;      | Indels 0 ;   | Gaps 0 ; |              |
| Qy                    | 1 MTDSVITYSMLELPATAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60        |                     |              |          |              |
| Db                    | 1 MTDSVITYSMLELPATAQNDYGPQQKSSSSXPSCSCLVATLGLITAVILSVLYQWIL 60        |                     |              |          |              |
| Qy                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |              |          |              |
| Db                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |              |          |              |
| Qy                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |              |          |              |
| Db                    | 61 CGGSNTSTCASCPCSPCPDRMKYGNHCHYFYSVEKDWNNSLEFCCLARDSHLLVITDNOEMS 120 |                     |              |          |              |
| Qy                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |              |          |              |
| Db                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |              |          |              |
| Qy                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |              |          |              |
| Db                    | 121 LLQVFLSSAFCWIGLRNNSGWEDGSPLNFSRISNSFVQTCGAINKNGLQASSCEVPL 180     |                     |              |          |              |
| Qy                    | 181 HGVCKKYRL 189   |                     |              |          |              |
| Db                    | 181 HGVCKKYRL 189   |                     |              |          |              |

|    |      |   |    |  |
|----|------|---|----|--|
| XX | WPI: | 2003-801317/75.   |    | RESULT 4   |
| XX | PT   | New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.   | ID | ABGG05451 standard; protein: 843 AA.   |
| XX | PT   | Disclosure: SEQ ID NO 196; 157pp; English.  | XX | ABGG05451;   |
| XX | CC   | The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain polypeptide contains capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide contains no more than one cysteine residue. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. | AC | ABGG05451;   |
| XX | CC   | The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030118532. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.   | XX | 13-FEB-2002 (first entry)  |
| XX | CC   | Sequence 189 AA;  | XX | Novel human diagnostic protein #5442.  |
| XX | CC   | Query Match 98.4%; Score 1007; DB 7; Length 189;  | DB | Novel human diagnostic protein #5442.  |
| XX | CC   | Best Local Similarity 98.4%; Pred. No. 8..56-97;  | XX | Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. |
| XX | CC   | Matches 186; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  | AC | ABGG05451;   |
| XX | CC   | QY 1 MTDSVITYSMELPTATQONDYGPQKSSSSRPSCLVAVITGLLTAVLLSVLVQWL 60  | XX | 13-MAR-2002  |
| Db | CC   | 1 MTDSVITYSMELPTATQONDYGPQKSSSSRPSCLVAVITGLLTAVLLSVLVQWL 60   | DT | (first entry)  |
| QY | CC   | 61 CGGSNYSTCASCPCSPCPDRMKYGNHCYYFSVEKDWNSSLEFLARDSHLLVTDNQEM 120  | XX | XX   |
| Db | CC   | 61 CGGSNYSTCASCPCSPCPDRMKYGNHCYYFSVEKDWNSSLEFLARDSHLLVTDNQEM 120  | XX | XX   |
| QY | CC   | 62 LLQYFLEAPFCWIGLRRNNSGWRWEDSPINEFSRISNSVQTCGAINKGLOSSCEVPL 180  | XX | XX   |
| Db | CC   | 121 LLQYFLEAPFCWIGLRRNNSGWRWEDSPINEFSRISNSVQTCGAINKGLOSSCEVPL 180   | XX | XX   |
| QY | CC   | 121 LLQYFLEAPFCWIGLRRNNSGWRWEDSPINEFSRISNSVQTCGAINKGLOSSCEVPL 180   | XX | XX   |
| Db | CC   | 181 HGVCKKVRL 189   | XX | XX   |
| QY | CC   | 181 HWVKCKVRL 189   | XX | XX   |
| Db | CC   | 725 SCPSCPDRMKYGNHCYYFSVEKDWNSSLEFLARDSHLLVTDNQEM 130   | XX | XX   |
| QY | CC   | 71 SCPSCPDRMKYGNHCYYFSVEKDWNSSLEFLARDSHLLVTDNQEM 130  | XX | XX   |
| Db | CC   | 665 ELPATAQONDYGPQKSSSSRPSCLVAVITGLLTAVLLSVLVQWL 724  | XX | XX   |

QY 131 CWIGLRRNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 169  
 Db 785 CWIGLRRNSGWRWEDGSPLNFSRISSNSFVOTCGAINKN 823

RESULT 5  
 AAE11760  
 ID AAE11760 Standard; protein; 188 AA.  
 AC AAE11760;  
 XX DT 18-DEC-2001 (first entry)  
 XX DR Mouse mast cell function associated antigen (MAFA) protein.  
 XX KW Pharmaceutical composition; mast cell function associated antigen;  
 KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
 KW immunosuppressive; cytosolic.  
 OS Mus sp.  
 XX PT  
 PH Key Location/Qualifiers  
 PT Domain 64 .188 /note= "Extracellular domain"  
 PT DN WO200170805-A2.  
 XX DD 27-SEP-2001.  
 XX DP 16-MAR-2001; 2001WO-US008596.  
 PR XX  
 PR 17-MAR-2000; 2000US-0190716P.  
 XX PA (GEMI-) GEMINI SCI INC.  
 PI XX  
 PI Takahashi N, Mikayama T;  
 DR XX  
 DR WPI; 2001-611482/70.  
 DR N-PSDB; AAD18735.  
 PT XX  
 PT Pharmaceutical composition for treating tumor by stimulating cytotoxic  
 PT activity of natural killer cell or T-cell, comprises an agent that binds  
 PT to mast cell function-associated antigen ligand on target cell.  
 XX PS Example 1: Page 19; 49pp; English.  
 CC The present invention relates to a pharmaceutical composition comprising  
 CC an agent which specifically binds to a mast cell function associated  
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA  
 CC ligand and a pharmaceutically acceptable excipient. The invention is  
 CC useful for inhibiting NK- or T-cell expressed cell surface MAFA  
 CC binding to a ligand on a target cell, by contacting the pharmaceutical  
 CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is mouse MAFA protein  
 XX SQ Sequence 188 AA.

QY 61 CGGSNYSTCASCPSCPDRWMKYGHNHCYXFVVEEKDNNSLEFCLARDSHLLVITDNGEMS 120  
 Db 61 CGGSKDKTSCPSCPILWTTNGSHCYXFSMEKQDSHLLTCPDQGVK 120

QY 121 LLQVFULEAFWIGLRRNSGWRWEDGSPLNFSRISSNSFVOTCGAINKNGLQASSCEVPL 180  
 Db 121 LFGEYLGQDFYWIGLNRNDGWRWEGLGPALS-LRILTNSLIQRGATHRNGLQASSCEVAL 179

QY 181 HGVCKKV 187  
 Db 180 QWICKKV 186

RESULT 6  
 AAR77033  
 ID AAR77033 standard; protein; 188 AA.  
 XX AC AAR77033;  
 XX DT 01-FEB-1996 (first entry)  
 XX DE Mammalian mast cell function-associated antigen (MAFA).  
 XX KW Mast cell function-associated antigen; MAFA; soluble; ligand;  
 KW identification; screening; inflammation; allergic; prevention.  
 XX OS Rattus ratus.  
 XX PN WO9527734-A1.  
 XX PD 19-OCT-1995.  
 XX PF 06-APR-1995; 95WO-US004258.  
 XX PR 08-APR-1994; 94IL-00109257.  
 XX PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (RYCU/ ) RYCUS A.  
 XX PI Pecht I, Guthmann MD, Tal M;  
 XX DR WPI; 1995-366356/47.  
 DR N-PSDB; AAI01471.  
 XX PS Novel DNA encoding a mast cell function-associated antigen (MAFA) -  
 PT Novel for screening for ligands of MAFA which are useful for prevention  
 PT of inflammatory and allergic reactions.  
 XX PS Claim 12; Page 37; 54pp; English.  
 XX SQ Query Match 51.4%; Score 525.5; DB 2; Length 188;  
 CC Best Local Similarity 53.5%; Pred. No. 1.7e-46;  
 CC Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  
 CC 1 MTDSVITYSMLEPTATAQANQDYGQQKSSSSKPSCSCLVAITGLITAVLISVLYQWIL 60  
 CC 1 MADNSIYSTLELPAAFPYQDDSRWKVAVLHRCPVSYLMVALLGLITVILMSLLYQRTL 60

Db 121 LLQVFULEAFWIGLRRNSGWRWEDGSPLNFSRISSNSFVOTCGAINKNGLQASSCEVPL 180  
 Db 121 CGGSKGFMCSQCSRCPNLWMRNGSHCYXFSMEKRDWNNSLKECADGSHLLTCPDQGVN 120

QY 1 MTDIVIYSMLEPTATAQANQDYGQQKSSSSKPSCSCLVAITGLITAVLISVLYQWIL 60  
 Db 1 MADSSIYSTLELPAAFPYQDDSRWKVAVLHRCPVSYLMVALLGLITVILMSLLYQRTL 60

Query Match 53.6%; Score 548.5; DB 4; Length 188;  
 Best Local Similarity 55.6%; Prod. No. 6.7e-49;  
 Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

QY 1 MTDSVITYSMLEPTATAQANQDYGQQKSSSSKPSCSCLVAITGLITAVLISVLYQWIL 60  
 Db 1 MADSSIYSTLELPAAFPYQDDSRWKVAVLHRCPVSYLMVALLGLITVILMSLLYQRTL 60

|  |   |  |
|--|---|--|
| Qy   | 181 HGVCKKV 187   | 121 LLQVFLSEAFCWIGLRNNSGWRWEQSPLNFSRISSSFVOTCGAINKNGIQLASSCERYPL 180             |
| Db   | 180 QWICCKV 186   | 121 LFQEYVGDFWIGLIRDIDGWRWEQSPALSLS-TILSNVVQKCGFTIHRCCGHASSCEVAL 179             |
| RESULT 7   |   |  |
| ID   | AAW88277  | AAW88277 standard; protein; 188 AA.  |
| XX   | AAW88277;   |  |
| XX   | DT 29-MAR-1999 (First entry)  |  |
| DE   | Rat mast cell function-associated antigen (MAFA).   |  |
| XX   | Mast cell function-associated antigen; MAFA; splice variant; rat;   |  |
| KW   | inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.   |  |
| XX   | Rattus sp.  |  |
| XX   | Key Location/Qualifiers   |  |
| FT Modified-site   | /note= "Asn is N-glycosylated"  |  |
| FT Modified-site   | 82. .84   |  |
| FT   | /note= "Asn is N-glycosylated"  |  |
| XX   | 97. .99   |  |
| FT   | /note= "Asn is N-glycosylated"  |  |
| XX   | WO954209-A2.  |  |
| XX   | 03-DEC-1998.  |  |
| XX   | 29-MAY-1998; 98WO-GB001572.   |  |
| PR   | 31-MAY-1997; 97GB-00011149.   |  |
| XX   | (PEPT-) PEPTIDE THERAPEUTICS LTD.   |  |
| PI   | Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  |  |
| XX   | WPI: 1999-059806/05.  |  |
| DR   | N-P5DB; AAV84222.   |  |
| XX   | New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.   |  |
| PS   | Disclosure; Fig 4; 44pp; English.   |  |
| XX   | This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW88265) and to the discovery of splice variants (see AAW88266-67) of human MAFA that are not found in rat. Polypeptides and synthetic peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g., rheumatoid arthritis and asthma), and tumour growth. |  |
| XX   | Sequence 188 AA;  |  |
| Query Match  | 51.4%   | Score 525.5; DB 2; Length 188;   |
| Best Local Similarity  | 53.5%   | Pred. No. 1.7e-46; Indels 1; Gaps 1;   |
| Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1; |   | Sequence 188 AA;   |
| Qy   | 1 MTDSVITYSMLELPATQANDYGPQQKSSSSKPSCSCLVAVITGLLTAVLLSYLIVYL 60  | Query Match 51.4%; Score 525.5; DB 4; Length 188;                                |
| Db   | 1 MADNSIYSTLELPAPRQVDDSRWKVAYLHRCPCSYLVNVALGLLTIVLMLLYQRTL 60   | Best Local Similarity 53.5%; Pred. No. 1.7e-46; Mismatches 29; Indels 1; Gaps 1; |
| Qy   | 61 CQGSNYSCTASCPCSPDRMKYGNHCYYSVEEEDWNSSLEFLCLARDSSLLVITDNQEMS 120  | 1 MTDSVITYSMLELPATQANDYGPQQKSSSSKPSCSCLVAVITGLLTAVLLSYLIVYL 60                   |
| Db   | 61 CGGSKGEMCSQCSRCPNLWMRNGSHCYYFSMKERDWNSSLUFCADKGSLLTFFDNQGW 120   | 1 MADNSIYSTLELPAPRQVDDSRWKVAYLHRCPCSYLVNVALGLLTIVLMLLYQRTL 60                    |
| Qy   | 61 CGGSNNYSTCASCPCSPDRMKYGNHCYYFSVEEEDWNSSLEFLCLARDSSLLVITDNQEMS 120  | 61 CGGSNNYSTCASCPCSPDRMKYGNHCYYFSVEEEDWNSSLEFLCLARDSSLLVITDNQEMS 120             |

|    |  |  |   |    |   |
|----|--|--|---|----|---|
| Db | 61 CGGSKGGMCSQCSRCPNLMNGSHCYFSMEKRDINNSLRFCA DRGSHLJTFP DNQGVN 120 | Qy   | 121 LLQVFLSEAFCWITGLRNNSGRWEDGSPLNFSRISNSFVQTGAINKNGLOSSCEVPL 180 | Qy | 121 LLQVFLSEAFCWITGLRNNSGRWEDGSPLNFSRISNSFVQTGAINKNGLOSSCEVPL 180 |
| Qy | 121 LLQVFLSEAFCWITGLRNNSGRWEDGSPLNFSRISNSFVQTGAINKNGLOSSCEVPL 180  | Db   | 64 -----  | Db | 64 -----  |
| Db | 121 LFQEYVGDFWIGLRLIDGWREDFPALSLS-TLSNSVIVQKCGTIRHCGLHASSCEVAL 179 | Qy   | 181 HGVCCKVRL 189   | Qy | 181 HGVCCKVRL 189   |
| Qy | 181 HGVCCKVRL 187  | Db   | 91 HWVCKVRL 99  | Db | 91 HWVCKVRL 99  |
| Db | 180 QWICEKV 186  |  |   |    |   |
|    |  | RESULT 10  |   |    |   |
|    |  | AAR77472   |   |    |   |
|    |  | ID AAR77472 standard; protein; 114 AA.                                       |   |    |   |
|    |  | XX   |   |    |   |
|    |  | AC AAR77472;   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | DT 01-FEB-1996 (first entry)   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | DE Partial sequence of mast cell function-associated antigen (MFAA).         |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Mast cell function-associated antigen; MFAA; soluble; ligand;                |   |    |   |
|    |  | KW KW identification; screening; inflammation; allergic;                     |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Mast cell function-associated antigen; MFAA; soluble; ligand;                |   |    |   |
|    |  | KW KW identification; screening; inflammation; allergic;                     |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Rattus rattus.   |   |    |   |
|    |  | OS XX  |   |    |   |
|    |  | PN WO9527734-A1.   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | PD 19-OCT-1995.  |   |    |   |
|    |  | XX   |   |    |   |
|    |  | PF 06-APR-1995;  |   |    |   |
|    |  | XX   |   |    |   |
|    |  | PR 08-APR-1994;  |   |    |   |
|    |  | XX   |   |    |   |
|    |  | (YEDA ) YEDA RES & DEV CO LTD.   |   |    |   |
|    |  | PA (RYCU/ ) RYCUS A.   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Pecht I, Guthmann MD, Tal M;   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | DR WPI: 1995-66356/47.   |   |    |   |
|    |  | DR N-PSDB; AAT01471.   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Novel DNA encoding a mast cell function-associated antigen (MFAA) -          |   |    |   |
|    |  | CC produced by recombinant techniques for use in the ligand- screening       |   |    |   |
|    |  | CC assay. The ligands that are identified may be used alone or in            |   |    |   |
|    |  | CC combination with the MFAA to prevent inflammatory and allergic reactions. |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Disclosure; Page 38; 54pp; English.  |   |    |   |
|    |  | PS   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | A soluble form of mast cell function-associated antigen (MFAA) -             |   |    |   |
|    |  | CC produced by recombinant techniques for use in the ligand- screening       |   |    |   |
|    |  | CC assay. The ligands that are identified may be used alone or in            |   |    |   |
|    |  | CC combination with the MFAA to prevent inflammatory and allergic reactions. |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Sequence 114 AA;   |   |    |   |
|    |  | SQ Disclosure; Fig 3; 44pp; English.   |   |    |   |
|    |  | PS   |   |    |   |
|    |  | This is the amino acid sequence of human mast cell function- associated      |   |    |   |
|    |  | PT PT function-associated antigen - useful in forming and manufacturing      |   |    |   |
|    |  | PT pharmaceutical compositions in the treatment of inflammatory and allergic |   |    |   |
|    |  | PT diseases, and tumour growth.  |   |    |   |
|    |  | XX   |   |    |   |
|    |  | This is the amino acid sequence of human mast cell function- associated      |   |    |   |
|    |  | CC antigen (MFAA) splice variant huMFA(E3/4-) , which lacks the C-lectin-    |   |    |   |
|    |  | CC like domain of human MFAA (See AAWB265) but retains the intracellular     |   |    |   |
|    |  | CC and transmembrane domains as well as the extracellular C-terminal tail.   |   |    |   |
|    |  | CC Truncated MFAA polypeptides including huMFA(E3/4-) and polynucleotides    |   |    |   |
|    |  | CC encoding them, as well as synthetic peptides (see AAW8238-64, AAW8268-    |   |    |   |
|    |  | CC 72), can be used be used in compositions for the treatment of             |   |    |   |
|    |  | CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and         |   |    |   |
|    |  | CC asthma), or tumour growth   |   |    |   |
|    |  | XX   |   |    |   |
|    |  | Sequence 99 AA;  |   |    |   |
|    |  | Query Match 42.1%; Score 431; DB 2; Length 99;                               |   |    |   |
|    |  | Best Local Similarity 50.3%; Pred. No. 5.4e-37;                              |   |    |   |
|    |  | Matches 95; Conservative 1; Mismatches 3; Indels 90; Gaps 1;                 |   |    |   |
|    |  | SQ   |   |    |   |
|    |  | 1 MTDSVITYSMELPLPATQAONDYGPQOKSSSKPSCSCLVIAITGLLTAVLLSVLYQNTL 60             |   |    |   |
|    |  | 1 MTDSVITYSMELPLPATQAONDYGPQOKSSSKPSCSCLVIAITGLLTAVLLSVLYQNTL 60             |   |    |   |
|    |  | Db   |   |    | RESULT 11   |
|    |  | 1 CQGSNSTCASCPCSPCPDRMKYGNHCYYSSVEEKDWNSSLEFCARDSHLVIITDNQEMS 120            |   |    | AAW8266   |
|    |  | Qy   |   |    | ID AAM8266 standard; protein; 70 AA.                              |
|    |  | 61 CQG-----  |   |    | XX  |
|    |  | Db   |   |    | AC AAM8266;   |
|    |  | 61 CQG-----  |   |    |   |
|    |  |  |   |    | 63  |

XX 29-MAR-1999 (first entry)

XX Human MAFA splice variant humMAFA (E3-) .

DE Human MAFA splice variant humMAFA (E3-) .

XX Mast cell function-associated antigen; MAFA; humMAFA (E3-); splice variant; human; inflammation; asthma; arthritis; tumour; therapy.

XX Homo sapiens.

OS Homo sapiens.

KW Human; NKp80; triggering NK; lymphoproliferative diseases; LDGL; lymphocyte.

XX Key Location/Qualifiers

XX Misc-difference 24 /note= "Encoded by CAA"

FT FT Misc-difference 43 /note= "Encoded by ACA"

FT FT Misc-difference 64 /note= "Encoded by CAG"

FT FT Misc-difference 158 /note= "Encoded by ATC"

FT XX EP1219637-A1.

EN PR 31-MAY-1997; 97GB-00011148.

PR 03-JUL-2002.

PD PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PF PF 29-MAY-1998; 98WO-GB001572.

XX XX 27-DEC-2000; 2000EP-00403689.

PR PR 27-DEC-2000; 2000EP-00403689.

XX XX 03-JUL-2002.

PA PA (INNA-) INNATE PHARMA.

PA (INNE-) UNIV GENOVA.

PI PI Moretta A, Bottino C, Biassoni R;

XX XX DR WPI; 2002-521944/56.

DR N-PSDB; ABQ78832.

PS SQ Sequence 70 AA;

PT New Polypeptide having a sequence corresponding to human mast cell function associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.

PT Disclosure; Fig 2; 44pp; English.

XX This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant humMAFA (E3-) . humMAFA (E3-) is a major transcript, not found in rat, but highly expressed in human lung and granulocyte-enriched blood cells. The truncated protein includes the intracellular and transmembrane regions of human MAFA (see AAWB8265), followed immediately by a polyproline motif (see AAWB8264) due to a reading frameshift. This unique motif has been used to design peptides (see AAWB8259-64, AAWB8268-72) that inhibit T cell antigen receptor-dependent activation induced by interleukin-2 (IL2) secretion from human Jurkat T cells or IgE dependent degranulation of rat basophil leukemic cells. Inhibition of IL2 production prevents T cell proliferation and suppresses the immune system. These preventives, truncated MAFA polypeptides including humMAFA (E3-), and polynucleotides encoding them, can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth.

CC Sequence 70 AA;

CC Query Match 30.0%; Score 306.5; DB 2; Length 70;

CC Best Local Similarity 82.9%; Pred. No. 3.5e-1; Mismatches 1; Indels 5; Gaps 1;

CC Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

QY 1 MTDYYIYSMELPATAQNDYGQQKSSSSKPSCTIVAITIGLILAVLSSVLYQWL 60

Db 1 MTDYYIYSMELPATAQNDYGQQKSSSSRPSCLIVIALGILAVLSSVLYQWL 60

QY 61 COGSNYSTCASPSCP 76

Db 61 CQ-----EPAPSFP 69

RESULT 12

ABBB1897 WNSSELEFCIARDSHLLVITDNQEMSLLOVFLSEA-FCWTIGLRNN--GWRNEDGSPFLN 151

ID ABBB1897 standard; protein; 231 AA.

XX AC ABBB1897;

XX DT 03-OCT-2002 (first entry)

XX DE Human NKp80.

XX SQ Sequence 231 AA:

Query Match 22.5%; Score 230; DB 5; Length 231;

Best Local Similarity 28.6%; Pred. No. 1.7e-15;

Matches 63; Conservative 32; Mismatches 61; Indels 64; Gaps 9;

QY 26 QKSSSKPKSCSCL-VAITI-----GILTAVLISVLY-----QWILCQG- 63

Db 15 KKRSQAQTSLFRDYSVTLHWKLLEISGTNGILTLISLILVSGVILKQRGGS 74

QY 64 -----SNYSTCASCPS------CPDRWMKGNHCYYFSVEKD 95

Db 75 CSNATQYEDGDLKVNNGTRRNKQKLCASRAADOTVLCQSEWLVK 134

QY 96 WNSSELEFCIARDSHLLVITDNQEMSLLOVFLSEA-FCWTIGLRNN--GWRNEDGSPFLN 151

Db 135 WSDSYVCLERKSLLIHDOLEMAFIQKNLRLQNLVYQNLNTSLAMTWTWDGSPID- 193

QY 152 SRISNSFVQ----TGGAINKNGLOSSCEVPLHGCK 185

Db 194 ---SKIFFKGPAKENSAKIKSETCSSVFRKWCQ 230

RESULT 13  
 PAM88815 standard; protein; 198 AA.  
 ID AAM88815;  
 XX  
 AC AAM88815;  
 XX  
 DT 07-NOV-2001 (first entry)  
 DE Human immune/haematopoietic antigen SEQ ID NO:16408.  
 XX  
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 cytostatic; gene therapy; vaccine; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157182-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US0001354.  
 XX  
 PR 31-JAN-2000; 2000US-0179005P.  
 PR 04-FEB-2000; 2000US-0180638P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189814P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198133P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214836P.  
 PR 30-JUN-2000; 2000US-0315155P.  
 PR 07-JUL-2000; 2000US-0216637P.  
 PR 07-JUL-2000; 2000US-0216830P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 14-AUG-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 14-AUG-2000; 2000US-0221683P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225233P.  
 PR 14-AUG-2000; 2000US-0225234P.  
 PR 14-AUG-2000; 2000US-0225236P.  
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 PR 14-AUG-2000; 2000US-0225447P.  
 PR 22-AUG-2000; 2000US-0225757P.  
 PR 23-AUG-2000; 2000US-0227112P.  
 PR 30-AUG-2000; 2000US-0225799P.  
 PR 01-SEP-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229279P.  
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 PR 06-SEP-2000; 2000US-0230438P.  
 PR 06-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
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 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.  
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 PR 14-SEP-2000; 2000US-0232399P.  
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 PR 17-NOV-2000; 2000US-0249207P.  
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 PR 17-NOV-2000; 2000US-0249210P.  
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 PR 17-NOV-2000; 2000US-0249212P.  
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 PR 17-NOV-2000; 2000US-0249244P.  
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 PR 17-NOV-2000; 2000US-0249246P.  
 PR 17-NOV-2000; 2000US-0249247P.  
 PR 17-NOV-2000; 2000US-0249249P.



PR 14-SEP-2000; 2000US-0232337P.  
 PR 14-SEP-2000; 2000US-0232338P.  
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 PR 14-SEP-2000; 2000US-0233033P.  
 PR 14-SEP-2000; 2000US-0233044P.  
 PR 14-SEP-2000; 2000US-0233055P.  
 PR 21-SEP-2000; 2000US-0233423P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234937P.  
 PR 25-SEP-2000; 2000US-0234938P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0235836P.  
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 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.

PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251968P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254057P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-465572/50.  
 DR N-PSDB; AAs31391.  
 XX  
 PT Nucleic acid molecules encoding human secreted extracellular matrix proteins used in preventing, treating or ameliorating a disorder, e.g., Alzheimer's and Parkinson's diseases and cancers.  
 PT  
 PT Proteins, used in preventing, treating or ameliorating a disorder, e.g., Alzheimer's and Parkinson's diseases and cancers.  
 XX  
 PS Claim 11; SEQ ID NO 470; 57pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g., humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to down regulate activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus), infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease), cardiovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary

Query Match 22.1%; Score 226; DB 4; Length 198;  
 Best Local Similarity 31.2%; Pred. No. 3.5e-15;  
 Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

Qy 44 GILTAVLISVLL--CWL--CQG-----SNTCAASCPS 74  
 Db 16 GILTLTLLSLLVSQCVLLKCQKGSCSNATQYEDTGDLKVNNGTRNNSNKDLGCSRSA 75

Qy 75 ---CPDRWVKYGNHCCYYFSEKVEKDWNSSLEFLCLARDSHULLTINQEMSLQVFLSEA 129  
 Db 76 DQTVLQSEWLLKQGKCYWFNEKMSWSDSVYCLERKSHULLIHPQLENAFIQKNLRLQ 135

Qy 130 -FCWIGLRNNs -GWRWEDGSPLNFSRISNSFVQ ---TCCAINRKNGLQASSCEVP 179  
 Db 136 NYWIGLNFETSLKMTKTWDGSPID ---SKIFFTKGPAKENSCAAIKESKICSETCSSV 191

Qy 180 LHGVCX 185  
 Db 192 FKWICQ 197

RESULT 15  
 ABP48040 ID ABP48040 standard; protein; 198 AA.

XX ABP48040;  
 AC ABP48040;  
 XX (POSE//) ROSEN C A.  
 PA (ROBE//) RUBEN S M.  
 DT (BARA//) BARASH S C.  
 XX DB Human polypeptide SEQ ID NO 470.  
 XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; antiviral;  
 KW anticarboxinolitan; antischick; antiaemic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antiallergic; antidiabetic; antidiulcer; anticonvulsant; antifungal;  
 KW antiparasitic; caridant; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
 XX OS Homo sapiens.  
 XX US2002042386-A1.  
 XX PD 11-APR-2002.  
 XX PP 17-JAN-2001; 2000US-00764870.  
 XX PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0189628P.  
 PR 28-MAR-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 11-JUL-2000; 2000US-0217487P.  
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 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
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 PR 30-AUG-2000; 2000US-0228386P.  
 PR 01-SEP-2000; 2000US-0228324P.  
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 PR 05-SEP-2000; 2000US-0229445P.  
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 PR 08-SEP-2000; 2000US-0229513P.  
 PR 21-SEP-2000; 2000US-0231413P.  
 PR 29-SEP-2000; 2000US-0234423P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 29-SEP-2000; 2000US-0234997P.  
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 PR 08-DEC-2000; 2000US-0251056P.  
 PR 08-DEC-2000; 2000US-0251968P.  
 PR 08-DEC-2000; 2000US-0251869P.

XX (ROBE//) ROSEN C A.  
 PA (ROBE//) RUBEN S M.  
 DT (BARA//) BARASH S C.  
 XX PI Rosen CA, Ruben SM, Barash SC;  
 XX DR WPI-2002-470713/50.  
 XX PI N-PSDB; ABQ6515.  
 XX PT New nucleic acid encoding human proteins, useful for diagnosis, treatment  
 PT and prevention of e.g. osteoporosis, also related polypeptides, and  
 PT antibodies.  
 XX PS Claim 11; SEQ ID NO 470; 235pp + Sequence Listing; English.  
 XX CC The invention relates to novel genes (ABQ6521-ABQ66785) and proteins  
 CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (anti)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing  
 CC ; (e) neurologic diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html?DocID=999909764870.  
 XX SQ Sequence 198 AA;

|                       |       |                    |                |             |
|-----------------------|-------|--------------------|----------------|-------------|
| Query Match           | 22.1% | Score 225;         | DB 5;          | Length 198; |
| Best Local Similarity | 31.2% | Pred. No. 3.5e-15; |                |             |
| Matches               | 58;   | Conservative 27;   | Mismatches 53; | Indels 48;  |
| Gaps                  | 8;    |                    |                |             |

QY 44 GLITPAVLLSVLTY--QWIL--COG-----SNYSTGASCPS 74  
 Db 16 GILITPLISLILLYSGLVLLKCQRGCSNATQYEDTGDLKVNNGTRRNISNKDLGASRRA 75

QY 75 -----CPDRWMKYGNHCVYESVFRDNSSLEFCUARDSHLLVTDQEMMSLIQYFLSEA 129  
 Db 76 DQTWLCQSEWLKYQCKCYWFSNENKWSDSYYCLERKSHLITHDQLENATIONRLQL 135

QY 130 -FCWIGLIRNS---GWRWEDGSPLNEFRTSSNSFVQ----TCAGAINKNGLOASCSCEVP 179  
 Db 136 NYVWWGLNTSLKMTWWDGSP1D---SKIFFKGPKAKENSAAIKSKIFPTCSSLV 191

QY 180 LHGVCK 185  
 Db 192 FKWICQ 197

Search completed: August 10, 2004, 16:16:27  
 Job time : 48.8319 secs

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.476;. Seconds (without alignments)

perfect score: 10/3 MTDSTVIYSMELPTATQAQN . . . . . GLQASSCEVPLHGVCKKVRL 189

Title: US-09-811-367B-1

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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3: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US06\_NEW\_PUB\_COMB.pep:\*

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7: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US08\_NEW\_PUB\_COMB.pep:\*

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9: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US09B\_PUBCOMB.pep:\*

10: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US09C\_PUBCOMB.pep:\*

11: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US09C\_PUBCOMB.pep:\*

12: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US09\_NEW\_PUB\_COMB.pep:\*

13: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US10A\_PUBCOMB.pep:\*

14: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US10B\_PUBCOMB.pep:\*

15: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US10C\_PUBCOMB.pep:\*

16: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US10\_NEW\_PUB\_COMB.pep:\*

17: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US60\_NEW\_PUB\_COMB.pep:\*

18: /cgn2\_6\_ptodata/2/pubpa/2/pubpa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

| Result No. | Score | Query Match | Length | DB ID                 | Description         |
|------------|-------|-------------|--------|-----------------------|---------------------|
| 1          | 1023  | 100.0       | 189    | 9 US-09-811-367B-1    | Sequence 1, Appli   |
| 2          | 1007  | 98.4        | 189    | 14 US-10-207-655-196  | Sequence 196, Appli |
| 3          | 548   | 53.6        | 188    | 9 US-09-811-367B-3    | Sequence 3, Appli   |
| 4          | 525   | 51.4        | 188    | 9 US-09-811-367B-5    | Sequence 5, Appli   |
| 5          | 230   | 22.5        | 231    | 16 US-10-457-843-1    | Sequence 1, Appli   |
| 6          | 226   | 22.1        | 198    | 9 US-09-764-870-470   | Sequence 470, Appli |
| 7          | 226   | 22.1        | 198    | 14 US-10-125-540-470  | Sequence 470, Appli |
| 8          | 226   | 22.1        | 203    | 9 US-09-764-870-309   | Sequence 309, Appli |
| 9          | 226   | 22.1        | 203    | 14 US-10-125-540-309  | Sequence 309, Appli |
| 10         | 217   | 21.2        | 35     | 9 US-09-864-761-33902 | Sequence 33902, A   |
| 11         | 216   | 21.2        | 182    | 9 US-09-764-870-310   | Sequence 33902, A   |
| 12         | 216   | 21.2        | 182    | 14 US-10-125-540-310  | Sequence 310, Appli |
| 13         | 201   | 19.6        | 225    | 15 US-10-377-127-25   | Sequence 25, Appli  |
| 14         | 196   | 19.2        | 179    | 15 US-09-919-039-130  | Sequence 130, Appli |
| 15         | 196   | 19.2        | 179    | 15 US-10-335-009-10   | Sequence 10, Appli  |

**ALIGMENTS**

RESULT 1 US-09-811-367B-1

; Sequence 1, Application US/09811367B-1

; Patent No. US20020155110A1

; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.

; ATTORNEY: Takahashi, No. US20020155110A1

; APPLICANT: Mikayama, Toshiyuki

; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MFAA)

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE

; FILE REFERENCE: 021286/0278719

; CURRENT APPLICATION NUMBER: US/09/811,367B

; CURRENT FILING DATE: 2002-03-12

; PRIORITY APPLICATION NUMBER: 60/190,716

; NUMBER OF SEQ ID NOS: 20

; SEQ ID NO: 1

; SOFTWARE: PatentIn version 3.0

; LENGTH: 189

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-811-367B-1

Query Match 100.0%; Score 1023; DB 9; Length 189;

Best Local Similarity 100.0%; Pred. No. 3.5e-97;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDSVIVSMLELTATQAQNDGQPKQKSSSKPSCLVAVITLGLTAVILSVLYQWIL 60

Db 1 MTDSVIVSMLELTATQAQNDGQPKQKSSSKPSCLVAVITLGLTAVILSVLYQWIL 60

QY 61 CGQSYNSTACSPCPDWMKYGNHCVFSVEEKDNSSLEFLARDSHLYTDTDQEMS 120

Db 61 CGQSYNSTACSPCPDWMKYGNHCVFSVEEKDNSSLEFLARDSHLYTDTDQEMS 120

QY 121 LIGQFVLSEAFCMIGLRNNSGWEDGSPLNFSRISNSFVOTCGAINKGLOASSCVP 180

Db 121 LIGQFVLSEAFCMIGLRNNSGWEDGSPLNFSRISNSFVOTCGAINKGLOASSCVP 180

RESULT 2  
US-10-2007-655-196  
; Sequence 196, Application US/10207655  
; Publication No. US2003011859A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069\_401CL  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 196  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-2007-655-196

Query Match 98.4%; Score 1007; DB 14; Length 189;  
Best Local Similarity 98.4%; Pred. No. 1.6e-95;  
Matches 186; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 MTDSVIYSMLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60  
Db 1 MTDSVIYSMLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60

Qy 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120  
Db 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120

Qy 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180  
Db 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180

Qy 181 HGVKCKV 189  
Db 181 HWVKCKV 189

RESULT 3  
US-09-811-367B-3  
; Sequence 3, Application US/09811367B  
; Patent No. US20020155110A1  
; GENERAL INFORMATION:  
; APPLICANT: GEMINI SCIENCE, INC.  
; APPLICANT: Takahashi, No. US20020155110A1  
; APPLICANT: Mikayama, Toshi Fumi  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)  
; FILE REFERENCE: 021286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811,367B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/190,716  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 9; Length 188;  
Best Local Similarity 53.5%; Pred. No. 6.7e-46;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60  
Db 1 MADNSIYSTLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60

Qy 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120  
Db 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120

Qy 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180  
Db 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180

Qy 181 HGVKCKV 187  
Db 180 QWICCKV 186

RESULT 4  
US-09-811-367B-5  
; Sequence 5, Application US/09811367B  
; Patent No. US20020155110A1  
; GENERAL INFORMATION:  
; APPLICANT: GEMINI SCIENCE, INC.  
; APPLICANT: Takahashi, No. US20020155110A1  
; APPLICANT: Mikayama, Toshi Fumi  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)  
; FILE REFERENCE: 021286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811,367B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/190,716  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 9; Length 188;  
Best Local Similarity 53.5%; Pred. No. 6.7e-46;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60  
Db 1 MADNSIYSTLEPDTAQNDYGPQQKSSSSKPSCSCLVAVTLGLITAVLVLVQWIL 60

Qy 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120  
Db 61 CGGSNTSTCASCSPCPDRMKYGNHCVYFSTEEKDNNSLEFCLARDSHLVLITDNQEMS 120

Qy 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180  
Db 121 LLQVFLSEAFCWIGLNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCEVPL 180

Qy 181 HGVKCKV 187  
Db 180 QWICCKV 186

RESULT 5  
US-10-451-843-1  
; Sequence 1, Application US/10451843  
; Publication No. US2004011578A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: Polypeptides having a triggering NK receptor activity and biolog  
; FILE REFERENCE: 1.249NKF80  
; CURRENT APPLICATION NUMBER: US/10/451,843  
; CURRENT FILING DATE: 2003-12-30

Query Match 53.6%; Score 548.5; DB 9; Length 188;  
Best Local Similarity 55.6%; Pred. No. 2.9e-48;  
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;



Db 197 FRWICQ 202

RESULT 9

US-10-125-540-309

; Sequence 309, Application US/101255540

; Publication No. US0030059875A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ14C1

; CURRENT APPLICATION NUMBER: US/10/125 540

; CURRENT FILING DATE: 2002-04-19

; PRIOR APPLICATION removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 646

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 309

; LENGTH: 203

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-125-540-309

Query Match 22.1%; Score 226; DB 14; Length 203;

Best Local Similarity 31.2%; Pred. No. 5.5e-15;

Matches 58; Conservative 27; Mismatches 53; Indels 48; Gaps 8;

SEQ ID NO: 33902

Length: 35

SOFTWARE: Amomax Sequence Listing Engine vers. 1.1

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Qy 44 GLTTAVILSVLVLVY-QMIL--CGG-----SNYSTCACPS 74

Db 21 GILTTLISLILIVSQVLLKCQKGSS-SNATQYEDTCDLKVNGLTRNNISNKDLCARSA 80

Qy 75 ----CDRMMKGNHCVYFSEEEKWDNSLFECLARDSHLVITDQEMSLQVFLSEA 129

Db 81 DDTVLCQSEWMLCTQGKYYFSEEMKSKSYDTSVYCLERKSHKLIIHDLEMFTAOKNLRL 140

Qy 130 -FCWIGLNNS --GWEWEDGSPLNFRRISNSFVQ----TCGAINKNGLQASSCEVP 179

Db 141 NYWGNINFNTSLKMTWVGDSPID---SKIFFKGPAKENSCAALESKIFSEICSSV 196

Qy 180 LRGVCK 185

Db 197 FRWICQ 202

Query Match 21.2%; Score 217; DB 9; Length 35;

Best Local Similarity 100.0%; Pred. No. 5.3e-15;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCACPSCPDRMKYGNHCVYFSVEEKDWNS 98

Db 1 SNYSTCACPSCPDRMKYGNHCVYFSVEEKDWNS 35

RESULT 11

US-09-864-761-33902

; Sequence 33902, Application US/09864761-

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Agomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864 761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR FILING DATE: 2000-06-30

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; OTHER INFORMATION: MAP TO AC007443.6.1

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.7

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.9

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.3

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22

; OTHER INFORMATION: EXPRESSED IN HEPATICA, SIGNAL = 8

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 30

; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.1

; OTHER INFORMATION: EST HUMAN HIT: BF41894.1, EVALU 4.00e-15

; OTHER INFORMATION: EST HUMAN HIT: AA188327.1, EVALU 1.00e-14

; OTHER INFORMATION: SWISSPROT HIT: PI4370, EVALU 3.00e-04

US-09-864-761-33902

Query Match 21.2%; Score 217; DB 9; Length 35;

Best Local Similarity 100.0%; Pred. No. 5.3e-15;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 SNYSTCACPSCPDRMKYGNHCVYFSVEEKDWNS 98

Db 1 SNYSTCACPSCPDRMKYGNHCVYFSVEEKDWNS 35

RESULT 12

US-09-764-870-310

; Sequence 310, Application US/09764870

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PTZ14

; CURRENT APPLICATION NUMBER: US/09/764,870

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 646

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 310

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-870-310

Query Match 21.2%; Score 216.5; DB 9; Length 182;

Best Local Similarity 35.0%; Pred. No. 4.6e-14;

Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5; US-10-379-127-25

Qy 64 SNYSTCASCPS---CPDRWMKGNHCYFSEVKDNMISLECLARDSHLLVITDQE 118 Query Match 19.6%; Score 201; DB 15; Length 225;  
Best Local Similarity 26.0%; Pred. No. 2, 4e-12;  
Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

Db 49 SNKDLCASRSADQTVLQCSPNFSRISNSFVQ---GWRWEDGSPLNFSRISNSFVQ---TCGAINK 168

Qy 119 MSLIQVFLSEA-FWIGLRRNS---GWRWEDGSPLNFSRISNSFVQ---TCGAINK 168 Qy 1 MTDPVIYSMLPELTATOQANDYGPQOKSSSKP-----SCSCLVAVITLG 44  
Db 109 MAFIQNLRLQNLVWIGLRTSLRMTWVDGSID---SKFFIKGFAKENSAAIKE 164 Db 1 MDQOAYAABLNT----DSCPSSSPSSLPDVCQSPHFOQALKLSCAGTLLVL- 53

Qy 169 NGLOSSSCCEVPLHGCK 185 Qy 45 LLTAFLVSVLYQWLQCGSNYSTCA-----SCPSCPDRWMKYGNNHXYFS 90  
Db 165 SKIFSETSSVFKWICQ 181 Db 54 VVTGLSVSTV---SLIQQSSSTERSYDQSQSRNKTKTERPGLINCPYWOOLREKCLLFS 109

RESULT 12

US-10-125-540-310 ; Sequence 310, Application US/09919039  
; Publication No. US20030198871A1

US-10-125-540-310 ; Sequence 310, Application US/10125540  
; Publication No. US20030059875A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

CURRENT APPLICATION NUMBER: US/10/125,540

CURRENT FILING DATE: 2002-04-19

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 646

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 310

LENGTH: 182

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-540-310

Query Match 21.2%; Score 216.5; DB 14; Length 182;  
Best Local Similarity 35.0%; Pred. No. 4.6e-14;  
Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

Qy 64 SNYSTCASCPS---CPDRWMKGNHCYFSEVKDNMISLECLARDSHLLVITDQE 118  
Db 49 SNKDLCASRSADQTVLQCSPNFSRISNSFVQ---GWRWEDGSPLNFSRISNSFVQ---TCGAINK 168

Qy 119 MSLIQVFLSEA-FWIGLRRNS---GWRWEDGSPLNFSRISNSFVQ---TCGAINK 168  
Db 109 MAFIQNLRLQNLVWIGLRTSLRMTWVDGSID---SKFFIKGFAKENSAAIKE 164

Qy 169 NGLOSSSCCEVPLHGCK 185  
Db 165 SKIFSETSSVFKWICQ 181

RESULT 13

US-10-379-127-25 ; Sequence 25, Application US/10379127  
; Publication No. US20040005592A1

GENERAL INFORMATION:

APPLICANT: Embage, Peter C.R.  
Dramanac, Radjoje

APPLICANT: Goodrich, Ryle

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAP  
FILE REFERENCE: NUVO-01CIP

CURRENT APPLICATION NUMBER: US/10/379,127  
CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 09/799,451

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 27

LENGTH: 225

TYPE: PRT

ORGANISM: Homo sapiens

US-10-335-009-10 ; Sequence 10, Application US/10335009  
; Publication No. US20040001804A1

GENERAL INFORMATION:

APPLICANT: Porteilloor, Mathew A.

TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION

FILE REFERENCE: 11707.02/4.69887-7

CURRENT APPLICATION NUMBER: US/10/335,009



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## OM protein - protein search, using sw model1

Run on: August 10, 2004, 16:13:57 ; Search time 14.7186 Seconds

(without alignments) 662.924 Million cell updates/sec

Title: US-09-811-367B-1

Perfect score: 1023

Sequence: 1 MTDSVYSMLELPATQAQN.....GLQASSCEVPLHGVCKKVRL 189

Scoring table: BLOSUM62

Gapext: 0.5

Searched:

389414 seqs., 5165971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cn2\_6/.ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cn2\_6/.ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/.ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cn2\_6/.ptodata/2/iaa/BOTUS\_COMB.pep:\*
- 6: /cgn2\_6/.ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description        |
|------------|-------|-------|-------|--------|-------------------|--------------------|
| 1          | 525.5 | 51.4  | 188   | 3      | US-09-722-126A-5  | Sequence 5, Appli  |
| 2          | 525.5 | 51.4  | 188   | 5      | PCT-US95-04258-5  | Sequence 5, Appli  |
| 3          | 430   | 42.0  | 76    | 4      | US-09-531-056A-23 | Sequence 23, Appli |
| 4          | 370.5 | 36.2  | 114   | 3      | US-08-722-126A-6  | Sequence 6, Appli  |
| 5          | 370.5 | 36.2  | 114   | 5      | PCT-US95-04258-6  | Sequence 6, Appli  |
| 6          | 201   | 19.6  | 225   | 2      | US-08-738-462-2   | Sequence 2, Appli  |
| 7          | 201   | 19.6  | 225   | 5      | PCT-US94-07587-2  | Sequence 2, Appli  |
| 8          | 196.5 | 19.2  | 179   | 1      | US-08-690-095-9   | Sequence 9, Appli  |
| 9          | 196.5 | 19.2  | 179   | 2      | US-08-650-578-2   | Sequence 2, Appli  |
| 10         | 196.5 | 19.2  | 179   | 3      | US-08-688-342-2   | Sequence 3, Appli  |
| 11         | 196.5 | 19.2  | 179   | 2      | US-09-113-788-3   | Sequence 3, Appli  |
| 12         | 196.5 | 19.2  | 179   | 3      | US-09-113-789-9   | Sequence 9, Appli  |
| 13         | 196.5 | 19.2  | 199   | 5      | PCT-US93-0418-4   | Sequence 4, Appli  |
| 14         | 193   | 18.9  | 270   | 2      | US-09-095-095-4   | Sequence 4, Appli  |
| 15         | 193   | 18.9  | 270   | 2      | US-08-809-494A-2  | Sequence 2, Appli  |
| 16         | 193   | 18.9  | 270   | 3      | US-09-352-302-2   | Sequence 2, Appli  |
| 17         | 193   | 18.9  | 273   | 2      | US-08-809-494A-4  | Sequence 4, Appli  |
| 18         | 193   | 18.9  | 273   | 3      | US-09-352-302-4   | Sequence 4, Appli  |
| 19         | 190   | 18.6  | 233   | 1      | US-08-690-095-8   | Sequence 8, Appli  |
| 20         | 190   | 18.6  | 233   | 1      | US-09-113-789-8   | Sequence 8, Appli  |
| 21         | 190   | 18.6  | 233   | 3      | US-08-543-246B-2  | Sequence 2, Appli  |
| 22         | 190   | 18.6  | 233   | 3      | US-08-543-246B-21 | Sequence 21, Appli |
| 23         | 185.5 | 18.1  | 316   | 3      | US-09-111-470-4   | Sequence 4, Appli  |
| 24         | 184   | 18.0  | 215   | 1      | US-08-690-095-7   | Sequence 7, Appli  |
| 25         | 184   | 18.0  | 215   | 3      | US-09-113-789-7   | Sequence 7, Appli  |
| 26         | 184   | 18.0  | 215   | 3      | US-08-543-246B-16 | Sequence 16, Appli |
| 27         | 184   | 18.0  | 215   | 3      | US-08-543-246B-22 | Sequence 22, Appli |

## ALIGNMENTS

|    |       |      |     |   |                   |                    |
|----|-------|------|-----|---|-------------------|--------------------|
| 28 | 182   | 17.8 | 231 | 1 | US-08-690-095-6   | Sequence 6, Appli  |
| 29 | 182   | 17.8 | 231 | 3 | US-09-113-789-6   | Sequence 6, Appli  |
| 30 | 182   | 17.8 | 231 | 3 | US-08-543-246B-6  | Sequence 23, Appli |
| 31 | 181   | 17.7 | 273 | 2 | US-09-095-095-3   | Sequence 3, Appli  |
| 32 | 181   | 17.7 | 273 | 2 | US-08-809-494A-6  | Sequence 6, Appli  |
| 33 | 181   | 17.7 | 273 | 3 | US-09-352-302-6   | Sequence 6, Appli  |
| 34 | 181   | 17.7 | 273 | 3 | US-08-543-246B-9  | Sequence 9, Appli  |
| 35 | 180   | 17.6 | 216 | 3 | US-08-543-246B-24 | Sequence 24, Appli |
| 36 | 180   | 17.6 | 216 | 3 | US-08-543-246B-24 | Sequence 10, Appli |
| 37 | 179.5 | 17.5 | 273 | 3 | US-09-111-470-10  | Sequence 10, Appli |
| 38 | 179.5 | 17.5 | 292 | 2 | US-08-688-342-4   | Sequence 4, Appli  |
| 39 | 179.5 | 17.5 | 292 | 2 | US-09-113-788-4   | Sequence 4, Appli  |
| 40 | 176   | 17.2 | 404 | 4 | US-09-517-605-2   | Sequence 17, Appli |
| 41 | 175.5 | 17.2 | 168 | 3 | US-08-772-440-17  | Sequence 17, Appli |
| 42 | 175.5 | 17.2 | 201 | 2 | US-09-113-788-1   | Sequence 1, Appli  |
| 43 | 175.5 | 17.2 | 201 | 2 | PCT-US93-10418-2  | Sequence 1, Appli  |
| 44 | 174   | 17.0 | 199 | 5 | PCT-US93-10418-2  | Sequence 2, Appli  |
| 45 | 173   | 16.9 | 175 | 3 | US-08-772-440-15  | Sequence 15, Appli |

|          |   |  |  |  |  |  |
|----------|---|--|--|--|--|--|
| RESULT 1 | US-08-722-126A-5  |  |  |  |  |  |
|          | ; Sequence 5, Application US/08722126A                    |  |  |  |  |  |
|          | ; GENERAL INFORMATION:                                    |  |  |  |  |  |
|          | ; Patent No. 603227                                       |  |  |  |  |  |
|          | ; APPLICANT: PECHT, Israel                                |  |  |  |  |  |
|          | ; GUTTMANN, Marcelo D.                                    |  |  |  |  |  |
|          | ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL |  |  |  |  |  |
|          | ; NUMBER OF SEQUENCES: 20                                 |  |  |  |  |  |
|          | ; CORRESPONDENCE ADDRESS:                                 |  |  |  |  |  |
|          | ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.                 |  |  |  |  |  |
|          | ; STREET: 419 Seventh Street N.W., Ste. 300               |  |  |  |  |  |
|          | ; CITY: Washington  |  |  |  |  |  |
|          | ; STATE: D.C.   |  |  |  |  |  |
|          | ; COUNTRY: UNITED STATES OF AMERICA                       |  |  |  |  |  |
|          | ; ZIP: 20004  |  |  |  |  |  |
|          | ; COMPUTER READABLE FORM:                                 |  |  |  |  |  |
|          | ; MEDIUM TYPE: Floppy disk                                |  |  |  |  |  |
|          | ; OPERATING SYSTEM: PC DOS/MS DOS                         |  |  |  |  |  |
|          | ; SOFTWARE: Patent Release #1.0, Version #1.30            |  |  |  |  |  |
|          | ; CURRENT APPLICATION DATA:                               |  |  |  |  |  |
|          | ; APPLICATION NUMBER: US/08/722,126A                      |  |  |  |  |  |
|          | ; FILING DATE: 08-OCT-1996                                |  |  |  |  |  |
|          | ; CLASSIFICATION: 536                                     |  |  |  |  |  |
|          | ; PTO/P application DATA:                                 |  |  |  |  |  |
|          | ; APPLICATION NUMBER: PCT/US95/04258                      |  |  |  |  |  |
|          | ; FILING DATE: 06-APR-1995                                |  |  |  |  |  |
|          | ; PRIOR APPLICATION DATA:                                 |  |  |  |  |  |
|          | ; APPLICATION NUMBER: IL 1.09257                          |  |  |  |  |  |
|          | ; FILING DATE: 08-APR-1994                                |  |  |  |  |  |
|          | ; ATTORNEY/AGENT INFORMATION:                             |  |  |  |  |  |
|          | ; NAME: BROWDY, Roger L.                                  |  |  |  |  |  |
|          | ; REGISTRATION NUMBER: 25, 618                            |  |  |  |  |  |
|          | ; REFERENCE/DOCKET NUMBER: PECHT-1A                       |  |  |  |  |  |
|          | ; TELECOMMUNICATION INFORMATION:                          |  |  |  |  |  |
|          | ; TELEPHONE: (202) 628-5197                               |  |  |  |  |  |
|          | ; TELEFAX: (202) 737-3528                                 |  |  |  |  |  |
|          | ; INFORMATION FOR SEQ ID NO: 5:                           |  |  |  |  |  |
|          | ; SEQUENCE CHARACTERISTICS:                               |  |  |  |  |  |
|          | ; LENGTH: 188 amino acids                                 |  |  |  |  |  |
|          | ; TYPE: amino acid  |  |  |  |  |  |
|          | ; TOPOLOGY: linear  |  |  |  |  |  |
|          | ; MOLECULE TYPE: protein                                  |  |  |  |  |  |
|          | ; US-08-722-126A-5  |  |  |  |  |  |
|          | ; Score 525.5, DB 3, Pred. No. 1.1e-48;                   |  |  |  |  |  |
|          | ; Best Local Similarity 53.5%;                            |  |  |  |  |  |

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLEPLTATAQNDYGPQOKPSSSKPSCSCLVAVLTGJLTAVLISVJLYWIL 60  
 1 MADNSIVSTLELPAAPIVQDDSRWKAVLHPCVSYLMVALGLITVILMSLLYQRTL 60

Db 61 CGGSNYSTCASCSPCPDRMKYGNHCYTFSVBKDNMSSLERCLARDSHLIVTQNEMS 120  
 61 CGGSKGFMCSQCSRCPNLMWRNGSHCYTFSMERKDNMSSLKFCAKGSHLJTFPDNGVN 120

Qy 121 LLQVFELSPAFCMGLRNSGWEWEDGSPNFSRISSSKPVQTCGAINKNGLOSSCEVPL 180  
 121 LQEYVYGEDFVWIGLRDIDGWEDGSPALSLISLNSSVQKCGTIRCGHLHASSEVAL 179

Db 121 HGVCCKV 187  
 121 QWICCKV 186

Qy 181 HGVCCKV 187  
 180 QWICCKV 186

Db RESULT 3  
 US-09-531-056A-23  
 ; Sequence 23, Application US/09531056A  
 ; Patent No. 6455683  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

Qy ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09/531-056A  
 ; CURRENT FILING DATE: 2000-03-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO: 23  
 ; LENGTH: 76  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-531-056A-23

Query Match 42.0%; Score 430; DB 4; Length 76;  
 Best Local Similarity 98.7%; Pred. No. 6e-39;  
 Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 PSCPDRWKYGNHCYTFSVBKDNMSSLERCLARDSHLIVTQNEMSLLGYOFSLAFCW 132  
 Db 1 PSCPDRWKYGNHCYTFSVBKDNMSSLERCLARDSHLIVTQNEMSLLQYFSLAFCW 60

Qy 133 IGLRNNSGWRWDGSP 148  
 Db 61 IGLRNNSGWRWDGSP 76

RESULT 4  
 US-08-722-126A-6  
 ; Sequence 6, Application US/08722126A  
 ; Patent No. 6034227  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PECHT, Israel  
 ; GUTHMANN, Marcelo D.  
 ; REFERENCE DOCUMENT NUMBER: TAL, Michael  
 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
 ; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 ; STREET: 419 Seventh Street N.W., Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 20004

Computer readable form:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

Current application data:  
 APPLICATION NUMBER: PCT/US95/04258  
 FILING DATE: 06-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 109257  
 FILING DATE: 08-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE DOCUMENT NUMBER: PECHT=1 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633

Information for seq id no: 5:  
 Sequence characteristics:  
 LENGTH: 188 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

PCT-US95-04258-5

Query Match 51.4%; Score 525.5; DB 5; Length 188;  
 Best Local Similarity 53.5%; Pred. No. 1.1e-48;  
 Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVIYSMLEPLTATAQNDYGPQOKPSSSKPSCSCLVAVLTGJLTAVLISVJLYWIL 60  
 1 MADNSIVSTLELPAAPIVQDDSRWKAVLHPCVSYLMVALGLITVILMSLLYQRTL 60

Db 61 CGGSNYSTCASCSPCPDRMKYGNHCYTFSVBKDNMSSLERCLARDSHLIVTQNEMS 120  
 61 CGGSKGFMCSQCSRCPNLMWRNGSHCYTFSMERKDNMSSLKFCAKGSHLJTFPDNGVN 120

Qy ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09531056A  
 ; Patent No. 6455683  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

Db ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09531056A  
 ; Patent No. 6455683  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

Qy ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09531056A  
 ; Patent No. 6455683  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

Db ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09531056A  
 ; Patent No. 6455683  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

FILING DATE: 08-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25, 618  
 REFERENCE/DOCKET NUMBER: PECHT-LA  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 114 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-722-126A-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;  
 Best Local Similarity 58.4%; Pred. No. 2.6e-32; Indels 1; Gaps 1;  
 Matches 66; Conservative 18; Mismatches 28;

QY 75 CPDRMKYGNHCVYYSVEKDWNSSLEFCLARDSHLLVITDQEMSLLQVLFSEAFCWIG 134  
 Db 1 CPNLWMRNGSHCYFSMERKDWNSLLKEFADKGSHLITFPDNQCNVLFPQEYVGDFYWG 60

QY 135 LRNNSGWRMEDGSPLNSFRISSPSVQTGAINKNGLOSSCEVPLHGCKV 187  
 Db 61 LRDIDGWRMEDGPALSLS-ILSNSYVQKCGTHRCGLHASCEVALQWCEKV 112

RESULT 6  
 US-08-738-462-2  
 Sequence 2, Application US/08738462  
 Patent No. 5965401  
 GENERAL INFORMATION:  
 APPLICANT: Chang, Chiwen  
 APPLICANT: Lanier, Lewis L.  
 APPLICANT: Phillips Jr., Joseph H.  
 TITLE OF INVENTION: Purified Mammalian NK Antigens and Related Reagents  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/738,462  
 FILING DATE: 16-JUL-1993  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA: US 08/093,435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Chiang, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0397  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-436-1200  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 225 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-738-462-2

Query Match 19.6%; Score 201; DB 2; Length 225;  
 Best Local Similarity 26.0%; Pred. No. 1.1e-13;  
 Matches 58; Conservative 36; Mismatches 81; Indels 48; Gaps 8;

QY 1 MTDSVIVSMLEYPTATAQGNDYGPQQSSSKP-----SCSCLVATLG 44  
 Db 1 MDQQAIIAYABNLPLP-----DSCPESSSPSLPRDVCGSPWHQFLAKLSAGLILVLY- 53

QY 45 LLTAVLLSVLTYLQMLCQSNYSTCA-----SCSCPDEWMKYGHNHCYVFS 90  
 Db 54 VVTGSDSVY---SLIQLSSSTEKPGLNCPYIWOQFLREKCLFS 109

QY 91 VEEXDWNSLEFCLARDSHLLVITDQEMSLLQVLFSEAFCWIG 187  
 Db 110 HTVNPNNSLADCSTESSLILLRDDELINTLIRDKAIFWGINFSLEKNNKWIN 169

Qy 146 GSPLNFS--RISSNSFPVOTCGAINKNLQASSEVPLHGVCKK 186  
 Db 170 GSFLNSDLEIRGDAKENSCISQTSEYCSSTEIRWICQK 212

## RESULT 7

PCT-US94-07587-2

; Sequence 2, Application PC/TUS9407587

; GENERAL INFORMATION:

; APPLICANT: Schering Corp.

; TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND

; TITLE OF INVENTION: RELATED REAGENTS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schering Corp.

; STREET: One Giralta Farms

; CITY: Madison

; STATE: New Jersey

; ZIP: 07940

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.1

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/TUS94/07587

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lunn, Paul G.

; REGISTRATION NUMBER: 32,743

; REFERENCE/DOCKET NUMBER: DX0397K

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-822-7255

; TELEFAX: 201-822-7039

; INFORMATION FOR SEQ ID NO: 2:

; INFORMATION CHARACTERISTICS:

; LENGTH: 225 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US94-07587-2

Query Match 19.6% Score 201; DB 5; Length 225;  
 Best Local Similarity 26.0%; Pred. No. 1..1e-13;  
 Matches 58; Conservative 36; MisMatches 81; Indels 48; Gaps 8;

1 MTDIVIYMLELPTAQNDYGPQQKSSSSXP-----SCSCLVAITLG 44

2 1 MDQQAIAAELNLPT-----DSPESSSPSSLPFRDVCGSPWHOFAKLKSCAGILILVL- 53

3 45 LITAVLISVLVYQWLKGNSNYSTCA-----SCPSCPDRWMKXGNHCYYS 90

4 54 VITGLSISVT---SLIQKSSIEKCSYDIQOSRNKTTERPGLINCPYWQDLREKCILFS 109

5 91 VEEKDWSLLEFLTARDLITDNEQMSLIQFLER--AFWIGR--NNSGWED 145

6 110 HTVNPWNNSLADGSTKSLLLRDKDELHTQNLIRKALFWIGLNFSLSERKWRWIN 169

7 146 GSPLNFS--RISSNSFPVOTCGAINKNLQASSEVPLHGVCKK 186

8 170 GSFLNSDLEIRGDAKENSCISQTSEYCSSTEIRWICQK 212

RESULT 8  
 US-08-690-095-9  
 ; Sequence 9, Application US/08690095  
 ; Patent No. 5792348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Au-Young, Janice

; ; APPLICANT: Goli, Surya K. HUMAN MACROPHAGE ANTIGEN  
 ; ; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 ; ; NUMBER OF SEQUENCES: 9  
 ; ; CORRESPONDENCE ADDRESS:  
 ; ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; ; STREET: 3174 Porter Drive  
 ; ; CITY: Palo Alto  
 ; ; STATE: CA  
 ; ; COUNTRY: U.S.  
 ; ; TIP: 94.04  
 ; ; COMPUTER READABLE FORM:  
 ; ; MEDIUM TYPE: Diskette  
 ; ; COMPUTER: IBM Compatible  
 ; ; OPERATING SYSTEM: DOS  
 ; ; SOFTWARE: Past-SEQ Version 1.5  
 ; ; CURRENT APPLICATION DATA:  
 ; ; APPLICATION NUMBER: US/08/690, 095  
 ; ; FILING DATE: Filed Herewith  
 ; ; ATTORNEY/AGENT INFORMATION:  
 ; ; NAME: Billings, Lucy J.  
 ; ; REGISTRATION NUMBER: 36,749  
 ; ; REFERENCE/DOCKET NUMBER: PF-0110 US  
 ; ; TELECOMMUNICATION INFORMATION:  
 ; ; TELEPHONE: 415-855-0555  
 ; ; TELEFAX: 415-845-4166  
 ; ; INFORMATION FOR SEQ ID NO: 9:  
 ; ; SEQUENCE CHARACTERISTICS:  
 ; ; LENGTH: 179 amino acids  
 ; ; STRANDEDNESS: single  
 ; ; TYPE: amino acid  
 ; ; IMMEDIATE SOURCE:  
 ; ; LIBRARY: GenBank  
 ; ; CLONE: 1098617  
 ; ; US-08-690-095-9  
 ; ; Query Match 19.2% Score 196.5; DB 1; Length 179;  
 ; ; Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
 ; ; Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;  
 ; ; Qy 35 CSCCLVATLGLLTAVLISVLVYQWLKGNSNYSTCA-----SCPSCPDRWMKXGNHCYYS 92  
 ; ; Db 20 CLSLIMA-TLGILLKNSFTKLSTEPAFTPGPNLIEQDSDCCSQQEKMVGRCNCYFISSE 78  
 ; ; Query Match 19.2% Score 196.5; DB 1; Length 179;  
 ; ; Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
 ; ; Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;  
 ; ; Qy 93 EKDWNSSLLEFLTARDLITDNEQMSLIQFLER--NNSGWED 145  
 ; ; Db 79 QKWNESPDHLCASQKSSLQDNTEDFMS--SSQEFWGLSYSEBHTAWLWNGSAI 136  
 ; ; RESULT 9  
 ; ; Sequence 2, Application US/08650578/2  
 ; ; Patent No. 5811284  
 ; ; GENERAL INFORMATION:  
 ; ; APPLICANT: Chang, Chiwen  
 ; ; APPLICANT: Aramburu Beltran, Jose  
 ; ; APPLICANT: Lopez-Bonet, Miguel  
 ; ; APPLICANT: Phillips Jr., Joseph H.  
 ; ; APPLICANT: Lanier, Lewis L.  
 ; ; TITLE OF INVENTION: Purified Mammalian NK Antigens and  
 ; ; RELATED REAGENTS  
 ; ; NUMBER OF SEQUENCES: 2  
 ; ; CORRESPONDENCE ADDRESS:  
 ; ; ADDRESSEE: DNAX Research Institute  
 ; ; STREET: 901 California Avenue  
 ; ; CITY: Palo Alto  
 ; ; STATE: California  
 ; ; COUNTRY: USA

ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/650,578  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/175,339  
 FILING DATE: 29-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0391  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 115-855-9196  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-650-578-2

Query Match 19.2%; Score 196.5; DB 2; Length 179;  
 Best Local Similarity 32.7%; Pred. No. 2.4e-13; Indels 15; Gaps 7;  
 Matches 53; Conservative 25; Mismatches 69; Insertions 15; Gaps 7;

QY 35 C\$CLVIAITIGLTLAVILSQQVFLSEAFKIGL--RNNSGMRWEDGSPL 149  
 DB 20 C\$LSIMA-TIGILLKNSFTLISIEAFTPGENIELQKDSCCS\$CQE\$KWCYRCNCYFISSE 78

QY 93 EKDWNSSLEFCLARDSHLLIVITDQNEM\$LQQVFLSEAFKIGL--RNNSGMRWEDGSPL 149  
 DB 79 QKTN\$EHL\$CASS\$LIQLQNTDELD\$MS--SSQ\$QF\$WIG\$YSE\$EHTAWLWENGSAL 136

QY 150 NFSRISNSNF---VQTGAINKNG-LQASSCEVPLHGVCK 186  
 DB 137 -SQYLFP\$FETNTKNCAYNPNGNALDE\$CDKNRYTICKQ 176

RESULT 10  
 US-08-650-342-3  
 Sequence 3, Application US/08688342  
 Patent No. 5871564  
 GENERAL INFORMATION:  
 APPLICANT: Au-Young, Janice  
 ADDRESS: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/688,342  
 FILING DATE: Filed Herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098616  
 US-08-688-342-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;  
 Best Local Similarity 32.7%; Pred. No. 2.4e-13; Indels 15; Gaps 7;  
 Matches 53; Conservative 25; Mismatches 69; Insertions 15; Gaps 7;

QY 35 C\$CLVIAITIGLTLAVILSQQVFLSEAFKIGL--RNNSGMRWEDGSPL 149  
 DB 20 C\$LSIMA-TIGILLKNSFTLISIEAFTPGENIELQKDSCCS\$CQE\$KWCYRCNCYFISSE 78

QY 93 EKDWNSSLEFCLARDSHLLIVITDQNEM\$LQQVFLSEAFKIGL--RNNSGMRWEDGSPL 149  
 DB 79 QKTN\$EHL\$CASS\$LIQLQNTDELD\$MS--SSQ\$QF\$WIG\$YSE\$EHTAWLWENGSAL 136

QY 150 NFSRISNSNF---VQTGAINKNG-LQASSCEVPLHGVCK 186  
 DB 137 -SQYLFP\$FETNTKNCAYNPNGNALDE\$CDKNRYTICKQ 176

RESULT 11  
 US-09-113-788-3  
 Sequence 3, Application US/09113788  
 Patent No. 5969104  
 GENERAL INFORMATION:  
 APPLICANT: Au-Young, Janice  
 ADDRESS: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,788  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/688,342  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-4166  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLOBE: 1098616  
 US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 3; Length 179;  
 Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVAVITLGLITAVILSLLQWLCOGSN-YSTCASCPSCPDRWMKYGNCYFYSVE 92  
 Db 20 CLSLMA-TLGILLNSFTKSIEPAFTPGPMIELQKSDCCSQCERKVGYRCNCYFISSE 78

Query Match 19.2%; Score 196.5; DB 2; Length 179;  
 Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVAVITLGLITAVILSLLQWLCOGSN-YSTCASCPSCPDRWMKYGNCYFYSVE 92  
 Db 20 CLSLMA-TLGILLNSFTKSIEPAFTPGPMIELQKSDCCSQCERKVGYRCNCYFISSE 78

RESULT 13  
 PCT-US93-10418-4

Query Match 19.2%; Score 196.5; DB 2; Length 179;  
 Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVAVITLGLITAVILSLLQWLCOGSN-YSTCASCPSCPDRWMKYGNCYFYSVE 92  
 Db 20 CLSLMA-TLGILLNSFTKSIEPAFTPGPMIELQKSDCCSQCERKVGYRCNCYFISSE 78

RESULT 13  
 PCT-US93-10418-4

GENERAL INFORMATION:  
 APPLICANT: Hjerrild, Kathryn A.  
 TITLE OF INVENTION: Activation Antigen CD669  
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10418

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Seese, Kathryn A.  
 REFERENCE/DOCKET NUMBER: 32,172

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

PCT-US93-10418-4

Query Match 19.2%; Score 196.5; DB 5; Length 199;  
 Best Local Similarity 27.2%; Pred. No. 2.7e-13;  
 Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;

Qy 17 QAONDYGPQ--QKSSSSSKPSCSCLVAVITLGLITAVILSLLQWLCOGSNYSCTGASCP 73  
 Db 18 RGGDHTATSIHFEKHHEG--SIOVSIPWAVLVLITSLITALIVNCKY---NCP 69

RESULT 12  
 US-09-113-789-9

Sequence 9, Application US/09113789  
 Patent No. 6034219

GENERAL INFORMATION:  
 APPLICANT: Au-Young, Janice L.  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Golli, Surya K.

TITLE: NOVEL HUMAN MACROPHAGE ANTIGEN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/113,789  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: PF-0110 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEXFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLOBE: 1098617  
 US-09-113-789-9

Qy 17 CEVPLHGVCCK 186

RESULT 15  
US-08-809-494A-2  
; Sequence 2, Application US/08809494A  
; Patent No. 5002250

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A;Residues: 1-257 <BER>  
 B;Cross-references: GB:MA8072; NID:9505324; PIDN:AAA48558.1; PMID:9505325  
 C;Superfamily: C-type lectin homology  
 F;129-241/Domain: C-type lectin homology <LCH>

Query Match 17.7%; Score 182; DB 2; Length 257;  
 Best Local Similarity 28.7%; Pred. No. 2.9e-10;  
 Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

Qy 3.2 RPHLSRPAVALG---LLTVILMSLIMYORIICCGSDSTSHCPCLWTRNSHCV 87  
 Db 86 RQNRRVLCVALSAVPCMVLAVAVLVRQPS---SPRPPPSHV---CPNAWVGFGQKCY 141

Qy 88 YFSMEEKDWNSSLKFCADKGSHLTFPDNGQVLFGEYLGRLNDG---WRME 144  
 Db 142 YFSDTEWSSEHCRGLASATLTDEEEMFLQYQPADRWLHRAEGDEHTWVA 201

Qy 145 GGPALSURLITNSL-----QRCGATHRNGLQASSECEVALQWICKK 185  
 Db 202 DGS-----FTNRPVFELRGGRCAVINGDGSSALCHSEKEFWCER 243

RESULT 4

Qy 100 LKPCADKGSHLTFPDNGQVLFGEYLGQDF---LYWIGLRLN----DGVWRWEGGPALS---L 151  
 Db 119 IVDGDGKGATMLQDDBELLFLDSIKEKNSLTKWLNSTLNSDVL 178

Qy 152 RILTNSLIQRCAATHRNGLQASSECEVALQWICKKVY 188  
 Db 179 KITGDTEENDSCAAISGDKVTFESCNSDNRWCQKELY 215

Qy JH0822 lymphocyte early activation antigen AIM/CD69 - human  
 Db Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 08-Oct-1999  
 C;Accession: JH0822; 156167; S60753  
 R;Lopez-Cabrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-Med, 178, 537-547, 1993  
 A;Title: Molecular cloning, expression, and chromosomal localization of the human early activating receptors.  
 A;Reference number: JH0822; MUID:93340630; PMID:8340758  
 A;Accession: JH0822  
 A;Molecule type: mRNA  
 A;Residues: 1-199 <RBS>  
 A;Cross-references: GB:Z22576; NID:9397938; PIDN:CAA80298.1; PID:9397939  
 A;Note: the authors translated the codon CAA for residue 110 as Glu  
 R;Hamann, J.; Piebig, H.; Strauss, M.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
 Eur. J. Immunol. 150, 4920-4927, 1993  
 A;Title: Expression cloning of the early activation antigen CD69, a type II integral membrane protein.  
 A;Reference number: I56167; MUID:9326703; PMID:8496594  
 A;Accession: I56167  
 A;Status: translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-199 <RBS>  
 A;Cross-references: GB:L0755; NID:9291897; PIDN:AB46259.1; PID:9291898  
 R;Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
 Eur. J. Immunol. 24, 1692-1697, 1994  
 A;Title: Structure of the gene coding for the human early lymphocyte activation antigen CD69.  
 A;Reference number: I56167  
 A;Accession: S60753  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-199 <SAN>  
 A;Cross-references: EMBL:Z30426; MUID:94298875; PMID:8026529  
 C;Comment: This protein is the earliest inducible cell surface glycoprotein expressed in T cells.  
 A;Gene: GDB:CD69  
 A;Cross-references: GDB:132925; OMIM:107273  
 A;Map Position: 12p13-12p12  
 C;KeyWords: glycoprotein; phosphoprotein; receptor; transmembrane protein  
 C;Superfamily: C-type lectin homology  
 F;39-64/Domain: C-type lectin homology <LCH>  
 F;85-194/Domain: C-type lectin homology <LCH>  
 F;18-30/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted  
 F;166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Qy 3 DSSYSTLELPAPQVQDESRWKLRKAVLHRPHLSR-----FAMYVALGLLRTVIM 51  
 Db 11 NSSLH---PESGQENDAT-----SPHESPRHEGSFQVPLCAVMVFFITLII 56

Query Match 16.9%; Score 173.5; DB 2; Length 199;  
 Best Local Similarity 23.8%; Pred. No. 1.5e-09;  
 Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

Qy 1 MADSSYSTLELPAPQVQDESRWKL---KAYLHRPHLSRFAMVALLL---TVILMSL 53  
 Db 1 MDTARVIFGLKPKRPTPGAWHESPPSLPPDACRPRRSRSLAKSCLAGLILLYVTGMSV 60

Qy 54 IMYQRIIIC-----CG-----SKBTSCTSHCPSCPILWTRNGSHCYFYSMEKKDNWNS 99  
 Db 61 LV-RVLIQKPSIBKCYVLIQENLNKTDCSALKCQDWLSHRDCKFHVSOVSNTWEEG 118

Qy 107 GSHLLTFPDNGQVLFGEYLGQDFFYWIGLRLNIDG-WRWEGGPALSIRI-LTNLSLQRCG 163  
 Db 117 GATLAVIDSEKDMNFLLRKYAGREEHVGLKKEPQHPWKNSKEFNFVNWTGGS--DKCV 174

|                 |  |  |  |
|-----------------|--|--|--|
| Qy              | 164 ATHRNGLQASSCEVALQWICKK 185<br>C;Species: Homo sapiens (man)  | Db   | 175 FLRNTEVSSMECEKKNLYWICNK 196<br>C;Accession: I38700   |
| <b>RESULT 5</b> |  |  |  |
| Qy              | hnKR-P1a protein - human<br>C;Species: Homo sapiens (man)  | Db   | 146 GPALSIRLITNLSLQRCGAITHRLQASSCEVALQWICK 184<br>C;Accession: I38700  |
| Qy              | R;Lanier, L.J.; Chang, C.; Phillips, J.H.<br>A;Title: Human NKR-P1a: A disulfide-linked homodimer of the C-type lectin superfamily encoding type I NK cell receptor group 2-C, splice form 1 - human<br>A;Status: Preliminary; translated from GB/EMBL/DBJ<br>A;Molecule type: mRNA<br>A;Residues: 1-225 <RES><br>A;Cross-references: EMBL:U11276; NID:9538270; PIDN:AAA21605.1; PMID:9544496<br>C;Superfamily: natural killer cell receptor P1; C-type lectin homology<br>F:94-210/Domain: C-type lectin homology <LCN> | Db   | 105 GTKLKYDKDREQEFLVSRVNNBWLMSMCGTTSFVCK 143<br>C;Accession: I38700  |
| <b>RESULT 6</b> |  |  |  |
| Qy              | Query Match 16.0% ; Score 164.5; DB 2; Length 225;<br>Best Local Similarity 27.4%; Pred. No. 1.3e-08;<br>Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;   | Db   | 1 MADSSSTLELP-EAPQ-----VQDESRWKLUKAVLHRPHLSRFAMYVALGL---45<br>1 MDDQAIAYELNLNPIDSGEASSPSSPLRPVCQGSPPHOPAL---KLSAGIILVLVFT 56<br>C;Accession: I38700  |
| Qy              | 46 -LTVILMSLIMYQRIICCG---SKDSTCSH--CPSCBILWTRNGSHCYYSFMSMEKKDN 97<br>Db  | 57 GLSVSVTSLIQKSSEIKEYSDVQSRNKTTERPGLNCPYQOLREXCLLFSHTVNPNW 116<br>C;Accession: I38700   |  |
| Qy              | 98 SSSLKFCAKGSHLLTFPNDQGVLFGEVIGQD---NIDGWRWEGGPALS- 150<br>Db   | 117 NSLADCSYKESSLILRKDEL-IHTQNLIRDKAFLWGLNFSLSEKWNKWINGSPFLNS 175<br>C;Accession: I38700 |  |
| Qy              | 151 -LRLITNLSLQRGATHERNGQASSCEVALQWICKV 187<br>Db  | 176 NDLBIRGDAKENSCISIOTSVSEYCSTEIRWICQKEL 214<br>C;Accession: I38700                     |  |
| <b>RESULT 7</b> |  |  |  |
| Qy              | JCT7135<br>A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom agkisacutacin beta chain precursor - sharp-nosed viper<br>A;Reference number: JCT7134; MUID:20025379; PMID:10559303  | Db   | T28141<br>C type lectin, B locus - chicken<br>C;Species: Gallus gallus (chicken)<br>C;Accession: T28141<br>R.Milne, S.; Kaufman, J.; Beck, S.<br>submitted to the EMBL Data Library, May 1998<br>A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex<br>A;Reference number: Z20475<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA<br>A;Residues: 1-156 <ML><br>A;Cross-references: EMBL:Al023516; NID:e1292539; PIDN:CAA18961.1<br>C;Genetics: Riec |
| <b>RESULT 8</b> |  |  |  |
| Qy              | Query Match 15.9% ; Score 163.5; DB 2; Length 146;<br>Best Local Similarity 30.2%; Pred. No. 1e-08;<br>Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;  | Db   | 126 NSCYTIGKERRRTWBSLLACTSKNSSLSDNEERIKFLASLIPSS--WIGVFRNSSHHP 183<br>C;Accession: T28141<br>R.Milne, S.; Kaufman, J.; Beck, S.<br>submitted to the EMBL Data Library, May 1998<br>A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex<br>A;Reference number: Z20475<br>A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A;Molecule type: DNA<br>A;Residues: 1-156 <ML><br>A;Cross-references: EMBL:Al023516; NID:e1292539; PIDN:CAA18961.1<br>C;Genetics: Riec               |

A;Map position: 16  
A;Introns: 17/1; 74/3; 110/2

Query Match 15.1%; Score 155.5; DB 2; Length 156;  
Best Local Similarity 25.0%; Pred. No. 6.7e-08;  
Matches 39; Conservative 24; Mismatches 68; Indels 25; Gaps 6;

Qy 39 AMVALGHITVILMSLIMYQRLICCGSKDSTCSH---CPSCPILWTRNGSHCYYSMEKK 95  
Db 3 AVFTVLITAYAFAVQFQ-----PHPQPACQPCPDWIGERGKCYXFSEDESN 50

Qy 96 WNSSLRKCADKGSHLITFPDNQGVKLGEYLQDFEYWLGNIDG---NRWEGGPAIS- 150  
Db 51 WTSSQNCSALGASIAVFDASDLSFTMRHKGSSTRRNWCTK 109

Qy 151 -LRITNLISIQRCGAHTHRNLQASSCCEVALWICK 185  
Db 110 LFQVQHGLI--CAVLDAGLSSHCSSTRRNWCTK 142

RESULT 9

JC4691 coagulation factor IX/factor X-binding protein chain A precursor - habu  
C;Species: Trimeresurus flavoviridis (habu)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Jun-2000  
R;Matsuzaki, R.; Yoshihara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.  
Biochem. Biophys. Res. Commun. 220, 382-387, 1996  
A;Title: cDNA cloning of IX/X-IP, a heterogeneous two-chain anticoagulant protein from s  
A;Reference number: JC4690; MUID:96184662; PMID:8655314  
A;Accession: JC4691  
A;Residues: 1-146 -MART1>  
A;Cross-references: DDBJ:D83332; NID:gi1402641; PIDN:BAA11888\_1; PID:gi1402642  
A;Experimental source: venom  
R;Atoda, H.; Hyuga, M.; Morita, T.  
J. Biol. Chem. 266, 14903-14911, 1991  
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate  
stein, tetrancetin, and lymphocyte FC epsilon receptor for immunoglobulin E.  
A;Reference number: A39332; MUID:91332000; PMID:1831197  
A;Accession: B39332  
A;Molecule type: protein  
A;Residues: 24-146 <AT0>  
R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.  
J. Biochem. 118, 965-973, 1995  
A;Title: Blood coagulant Factor IX-binding protein from the venom of Trimeresurus flav  
A;Reference number: JC4329; MUID:96318509; PMID:8749314  
A;Accession: JC4330  
A;Molecule type: protein  
A;Residues: 24-146 <AT2>  
C;Superfamily: tetraectin; C-type lectin homology  
C;Keywords: anticoagulant; blood coagulation; lectin; venom  
F;-1-3/Domain: signal sequence #status predicted <IG>  
F;24-146/Product: factor IX/X binding protein chain B #status predicted <IG>  
F;25-36/Domain: C-type lectin homology <LCH>  
F;25-36,53-142,119-134/Disulfide bonds: #status predicted

Query Match 14.8%; Score 152.5; DB 2; Length 146;  
Best Local Similarity 24.5%; Pred. No. 1.2e-07;  
Matches 39; Conservative 25; Mismatches 70; Indels 25; Gaps 5;

Qy 35 LSRFAMVALGLITVILMSLMYQRLICCGSKDSTCSHCPSCPILWTRNGSHCYYSMEKK 94  
Db 1 MGRFISNGFGLVFL-----SLSGTAAACPSD---NSSYEGHICYKPFSEPK 44

Qy 95 DNNSSLKPCADK-GSHLLTPFDNQ---VKLEGFLYQDFEWIGLRLN---DGWRWEG 145  
Db 45 NWADAENFCTOQHAGGLVLFQSEERADVFVYKLAQFGHSIFWGMISNYWNQCNWOSN 104

Qy 146 GPDSLITLNLIQRGAHTHRNLQASSCCEVALWICK 184  
Db 105 AAMILRYKAWAEBSYCVFFKSTNNKRSRACRMMAQFYCE 143

RESULT 10

T42710 mannose receptor, macrophage - mouse  
N;Alternative names: lambda lectin; phosphohiilipase A2 receptor  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jun-2000  
C;Accession: T42710  
R;Wu, K.; Yuan, J.; Lasky, J.A.  
J. Biol. Chem. 271, 21323-21330, 1996  
A;Title: Characterization of a novel member of the macrophage mannose receptor type C 1  
A;Reference number: Z222235; MUID:3635501; PMID:8702911  
A;Accession: T42710  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-147 9 <WUK>  
A;Cross-references: EMBL:U56734; NID:gi1336073; PIDN:AC52729\_1  
C;Superfamily: phosphohiilipase A2 receptor; C-type lectin homology; fibronectin type II repeat  
C;Keywords: membrane protein; receptor  
F;186-227/Domain: fibronectin type II repeat homology <2FR>

Query Match 14.8%; Score 152.5; DB 2; Length 1479;  
Best Local Similarity 32.0%; Pred. No. 1.4e-06;  
Matches 48; Conservative 12; Mismatches 59; Indels 31; Gaps 8;

Qy 66 DSTCSHCPSCPILWTRNGSHCYYSMEKKDNWNSSLKFCADKGSHLIT-----112  
Db 659 DPTPSLTGSCPQGWTSDFDPKLRHCKYKVSSERLQEKWSWIALGVCRELGQQLSLASYEE 718  
Db 113 --FPDNQGVKLFG---EYLQDFWYIGLRLNID---GWRWEGGPALSRLRLTNSL---158  
Db 719 BHFAVHMLNKIFGESESREPBESHQHWFWIGLNRDPREGHSNRWDGLGFSYHFNRSRHDD 778

Query Match 14.8%; Score 152.5; DB 2; Length 1479;  
Best Local Similarity 32.0%; Pred. No. 1.4e-06;  
Matches 48; Conservative 12; Mismatches 59; Indels 31; Gaps 8;

Qy 159 -IQRGAHTHRNLQ---ASCEVAIWICK 184  
Db 779 DDIRGCAVLDLASLQWVPMQCTQIWIICK 808

RESULT 11

PR0372 natural killer cell receptor group 2, splice form A - human  
N;Alternative names: NK2-A; NK2-B  
N;Contains: natural killer cell receptor group 2, splice form B  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-May-2000  
C;Accession: PR0372; PT0373  
R;Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.  
J. Exp. Med. 173, 1017-1020, 1991  
A;Title: DNA sequence analysis of NK2, a family of related cDNA clones encoding type I  
A;Reference number: PR0372; MUID:91178434; PMID:2007850  
A;Accession: PR0372  
A;Molecule type: mRNA  
A;Residues: 1-233 <HOUL>  
A;Cross-references: EMBL:X54867; NID:gi35056; PIDN:CAA38649\_1; PMID:935057  
A;Experimental source: natural killer cell  
C;Genetics:  
A;Gene: GDB:KLRC1; NK2  
A;Cross-references: GDB:138773; OMIM:161555  
A;Map\_Protein: natural killer cell receptor P1; C-type lectin homology  
C;Superfamily: natural killer cell receptor group 2, splice form B  
C;Keywords: alternative splicing; glycoprotein; transmembrane protein  
F;71-98/Domain: C-type lectin homology <LCR>  
F;119-229/Domain: C-type lectin homology <LCR>  
F;102,103,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;119-130,147-229,208-221/Disulfide bonds: carbohydrate (Asn) (covalent) #status predicted  
Query Match 14.7%; Score 151; DB 2; Length 233;  
Best Local Similarity 23.0%; Pred. No. 2.8e-07;

Matches 45; Conservative 29; Mismatches 86; Indels 36; Gaps 6; C;Keywords: transmembrane protein F:34-210/Domain: C-type lectin homology <LCH>

Query Match 14.5%; Score 149; DB 2; Length 223;  
Best Local Similarity 22.8%; Pred. No. 4.2e-07;  
Matches 49; Conservative 36; Mismatches 90; Indels 40; Gaps 8;

QY 7 YSTLELPAPQVQDESRWKUKAVLHRPHLSRFAAMVALGILITVIL-  
Db 59 YHCKDLPSSAE-----KLIVGILGLICLIMASVTVVTPSTLILQ 99  
C;Species: Mus musculus (house mouse)  
Db 56 YQLLCGGSKDSTSCHCSPILWTRNGSHCYYFSMEKDWNSLLKFCADKGSHLLTFD 115  
C;Species: Mus musculus (house mouse)  
Db 100 RHNNSSLNTRTQKARHCGHGCGPEENITYSSCSCYIGKERLTWEELACTSKNSLLISIN 159  
C;Species: Mus musculus (house mouse)  
Qy 116 NQGVKLFGFEGYLQDFWYIGH--RNIDGWWRW-EGGPALSRLTNLSLQ RCGAHLHRNGCQ 171  
C;Species: Mus musculus (house mouse)  
Db 160 EEEKFLS--IISPSSEWIGVFRNSSHHPWTMNGLAFAKEIKUDSDNAEILCAVLQVNARIK 217  
C;Species: Mus musculus (house mouse)  
Qy 172 ASSCEVALQWICKYKL 187  
C;Species: Mus musculus (house mouse)  
Db 218 SAQCGSSIIYHCKHKL 233  
C;Species: Mus musculus (house mouse)

RESULT 1.2

S4719 phospholipase A(2) receptor protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 07-May-1995 #sequence\_revision 21-Jun-1995 #text\_change 20-Jun-2000  
C;Accession: S48719  
R;Igashino, K.; Ishizaki, J.; Ohara, O.; Arita, H.  
Bur. J. Biochem. 225, 375-382, 1994  
A;Title: Structural comparison of phospholipase A(2)-binding regions in phospholipase-A  
A;Reference number: S48719; MUID:95010128; PMID:7925549  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Cross-references: GB:D30779; NID:gi1375042; PID:BA006443\_1; PID:9691754  
C;SuperFamily: phospholipase A2 receptor; C-type lectin homology; fibronectin type II repeat  
F:180-503/Domain: C-type Lectin homology <LCH>

Query Match 14.7%; Score 151; DB 2; Length 1487;  
Best Local Similarity 27.0%; Pred. No. 2e-06; Mismatches 21; Indels 67; Gaps 9;  
Matches 43; Conservative 21; Mismatches 67; Indels 28; Gaps 9;

QY 57 QRLUCGS----KDSTCSHCP-----CPILWTRNGSH--CYYFS MEKKDNNSLL 101  
Db 202 EHLLNCATTSRYSERDEKNGFCPDPDTSMKYCFCDATWORNSRRCYQFLNSSL SWNQDHS 261  
C;Species: Mus musculus (house mouse)  
Qy 102 FCADKGSHLLTFPDNQGTVLFGWYLGQ--DFYWLGLRNID--GWRWEGGPALSL--- 151  
Db 262 SCLMOGGALSIATAEDDEFIREKHLSKVYKEYWNLQNLDEKAGWQWSDGTPLSYLNWSQ 321  
C;Species: Mus musculus (house mouse)  
Qy 152 RILTNSLIQ--RCGAH--RNGLOASSCEVALQWICKYKL 187  
Db 322 EITPGPFVHHCGTLEVVSAAWRSDCESTLPICKRDL 360  
C;Species: Mus musculus (house mouse)

RESULT 1.3

B4467 NKR-P1 protein homolog - mouse  
C;Species: Mus musculus (house mouse)  
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill  
A;Reference number: A44667; MUID:9134596; PMID:1880421  
A;Accession: B44667  
A;Molecule type: mRNA  
A;Residues: 1-223 <G1o>  
A;Cross-references: GB:M77677; NID:9200060; PID:AAA339823\_1; PID:9200061  
A;Experimental source: NK cells, C57BL/10  
A;Note: sequence extracted from NCBI backbone (NCBIN52380, NCBIPI:52381)  
C;Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match 14.5%; Score 149; DB 2; Length 223;  
Best Local Similarity 22.8%; Pred. No. 4.2e-07;  
Matches 49; Conservative 36; Mismatches 90; Indels 40; Gaps 8;

QY 6 IYSTLELPAPQVQDESRWKUKAVLHRPHLSRFAAMVALGILITVILMSL 53  
Db 7 VYADDLNLRQIQEPRHDSPSLSPDTCRPWR-----IRLAL-KFGCAGLILILVUVICL 59  
C;Species: Homo sapiens (man)  
Db 54 LM-----YQILCCGSKDST-----CSHCPSCPILWTRNGSHCYYFSMEKKDNNSLL 100  
C;Species: Homo sapiens (man)  
Db 60 CVLVLSVQKSSVOKICADYOENRTHTDCSVNLCEPODWLSHRDKCFRVQSVNTWEEQ 119  
C;Species: Homo sapiens (man)  
Qy 101 KFCADKGSHLLTFDQNQYVQLFEGYLQDF--YWIGLRLNID--DGWRWEGGPALS---LR 152  
C;Species: Homo sapiens (man)  
Db 120 ADGCRKGATLILLIQDQEELRFLDSIKEVYKNSTWIGLRTLPDMNWKWINGTIFNSDVLK 179  
C;Species: Homo sapiens (man)  
Qy 153 ITLNSLQIQRGAGATHRGLOASSCEVALQWICKYKL 187  
Db 180 ITGDIENGSCAS1SGDKVTSESCSTDNRWICREL 214  
C;Species: Homo sapiens (man)

RESULT 1.4

HIV SP120-binding C-type lectin - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-1995  
C;Accession: A46274  
R;Curtis, B.M.; Scharnowski, S.; Watson, A.J.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992  
A;Title: Sequence and expression of a membrane-associated C-type lectin that exhibits C-type lectin homology <LCH>  
A;Reference number: A46274  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-404 <CUR>  
A;Experimental source: Placenta  
A;Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIPI:113135)  
C;Superfamily: C-type lectin homology  
F:256-377/Domain: C-type Lectin homology <LCH>

Query Match 14.5%; Score 149; DB 2; Length 404;  
Best Local Similarity 25.8%; Pred. No. 7.9e-07;  
Matches 49; Conservative 29; Mismatches 8; Indels 30; Gaps 8;

QY 11 ELPEAPQYD--ESRKLUKAVLHRPHLSRFAAMVALGILITVILMSL MYQRLCGSKDST 68  
Db 205 ELPKSKQOEIYQELTRKA-----AVGELPEKSQOEIYQEL--TQLKAV 249  
C;Species: Homo sapiens (man)  
Qy 127 QDQFWYIGLRLNID--GPRW-EGGPALSL-----RILTNSLQIQR-CGAHNRNGQASSC 175  
Db 310 SNRFTWGLSLDNQETGTWQWDGSPLLPSFKQYWNRGEPNVGEEDCAEFSGNGWNDDKC 369  
C;Species: Homo sapiens (man)  
Db 176 EVALQWICKK 185  
C;Species: Homo sapiens (man)  
Db 370 NLAXFWICKK 379  
C;Species: Homo sapiens (man)

RESULT 1.5

A43532 B-cell surface antigen CD72 - human  
A;Title: A-15  
A;Status: preliminary  
A;Accession: A43532  
A;Molecule type: protein  
A;Residues: 1-223 <G1o>  
A;Cross-references: GB:M77677; NID:9200060; PID:AAA339823\_1; PID:9200061  
A;Experimental source: NK cells, C57BL/10  
A;Note: sequence extracted from NCBI backbone (NCBIN52380, NCBIPI:52381)  
C;Superfamily: natural killer cell receptor P1; C-type lectin homology

C;Date: 28-Oct-1992 #sequence\_revision 28-Oct-1992 #text\_change 21-Jul-2000  
C;Accession: A43532  
R;von Hoegen, I.; Nakayama, E.; Parnes, J.R.  
J. Immunol. 144, 4870-4877, 1990

A;Title: Identification of a human protein homologous to the mouse Lyb-2 B cell differentiator  
A;Reference number: A43532; MUID:9028102; PMID:2141045  
A;Accession: A43532  
A;Molecule type: mRNA  
A;Residues: 1-159 <VCN>  
A;Cross-references: GB: M54992; NID: 9187262; PIDN: AAA36189.1; PID: g187263  
C;Genetics  
A;Gene: GDB: CD72  
A;Cross-references: GDB: 128153; OMIM: 107272  
A;Map position: 9p-9p  
C;Superfamily: C-type lectin homology  
C;Keywords: B-cell; glycoprotein; homodimer; surface antigen; transmembrane protein  
F;1-95 /Domain: intracellular #status predicted <CYT>  
F;96-116 /Domain: transmembrane #status predicted <TM>  
F;117-359 /Domain: extracellular #status predicted <EXT>  
F;136 /Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match Score 147.5; DB 2; Length 359;  
Best Local Similarity 27.3%; Pred. No. 9.7e-07;  
Matches 38; Conservative 19; Mismatches 61; Indels 21; Gaps 6;  
Qy 62 CGSKDSTCSHCPSCPITIWTNGSHCYFSMEKDKWNSLTKCADKGSHLTF----PDNQ 117  
Db 226 CGSAD-TC----CPSWIMROKSCFVISLTSKNWSOKOCETLSKLATFSEYTPQSH 279  
Qy 118 GVKLFGEYL---GQDFYWGILRNIDQWRWEGGPALSRLITNSLQRCGAHRN---G 169  
Db 280 SYYFLNSLPLNGSGNSYWTGLSSNKDWKLTD----TQRTRTYAQS SKCNRVHKTWSSWT 336  
Qy 170 IQASSCEVALWICKVLY 188  
Db 337 LESESCESSSLPYICEMTAF 355

Search completed: August 10, 2004, 16:19:36  
Job time : 12.9788 secs

| Result No. | Score | Query  | Match  | Length | DB ID       | Description              |
|------------|-------|--|--------|--------|-------------|--------------------------|
| 1          | 180.5 | BLOSUM62   | 179    | 1      | CD94_MACMU  | Q9mz9 macaca mulu        |
| 2          | 180.5 | Gapop 10.0 , Gapext 0.5  | 227    | 1      | CD94_MOUSE  | P27811 mus musculu       |
| 3          | 178.5 | Total number of hits satisfying chosen parameters:   | 141681 | 1      | CD94_HUMAN  | Q13241 homo sapien       |
| 4          | 178.5 | Minimum DB seq length: 0   | 179    | 1      | CD94_PANTR  | Q07108 homo troglod      |
| 5          | 173.5 | Maximum DB seq length: 2000000000  | 179    | 1      | CD69_HUMAN  | P37717 mus musculu       |
| 6          | 168   | Post-processing: Maximum Match 100%  | 199    | 1      | CD69_MOUSE  | Q9gne8 pan troglod       |
| 7          | 168   | Listing First 45 summaries   | 199    | 1      | NKG_C_PANTR | P26717 homo sapien       |
| 8          | 158.5 | Database : SwissProt_42:*  | 233    | 1      | NKG_G_HUMAN | Q95ni5 pan troglod       |
| 9          | 158   | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | 231    | 1      | NKG_A_PANTR | P23807 trimers           |
| 10         | 152.5 | SUMMARIES  | 146    | 1      | IXB_TRIFL   | P26715 homo sapien       |
| 11         | 151   | Scoring table: BLOSUM62  | 233    | 1      | NKG_A_HUMAN | Q93427 crotalus dur      |
| 12         | 150.5 | Gapop 10.0 , Gapext 0.5  | 148    | 1      | CYXB_CRODU  | P27812 mus musculu       |
| 13         | 149   | Total number of hits satisfying chosen parameters:   | 223    | 1      | NK12_MOUSE  | Q9mz9 macaca mulu        |
| 14         | 148   | Minimum DB seq length: 0   | 216    | 1      | NKGD_MACMU  | Q9mz9 macaca mulu        |
| 15         | 147.5 | Maximum DB seq length: 2000000000  | 359    | 1      | CD72_HUMAN  | P21854 homo sapien       |
| 16         | 146.5 | Post-processing: Maximum Match 100%  | 233    | 1      | NKGE_PANTR  | P14371 fowlpox vir       |
| 17         | 146.5 | Listing First 45 summaries   | 163    | 1      | IXB_TRIFL   | P27811 rattus norvegicus |
| 18         | 146   | Database : SwissProt_42:*  | 223    | 1      | NK14_MOUSE  | P27814 mus musculu       |
| 19         | 145   | Scoring table: BLOSUM62  | 146    | 1      | MMHB_AKGHA  | Q9y192 agkistrodon       |
| 20         | 144   | Gapop 10.0 , Gapext 0.5  | 149    | 1      | CLE2_HUMAN  | Q92478 homo sapien       |
| 21         | 144   | Total number of hits satisfying chosen parameters:   | 216    | 1      | NKGD_HUMAN  | P26118 homo sapien       |
| 22         | 144   | Minimum DB seq length: 0   | 167    | 1      | NKGE_PANTR  | Q07444 homo sapien       |
| 23         | 144   | Maximum DB seq length: 2000000000  | 240    | 1      | LECI_MOUSE  | P24121 mus musculu       |
| 24         | 139.5 | Post-processing: Maximum Match 100%  | 231    | 1      | NKG_C_MACMU | Q9mz9 macaca mulu        |
| 25         | 139   | Listing First 45 summaries   | 157    | 1      | MMHG_AKGHA  | Q9y199 agkistrodon       |
| 26         | 139   | Database : SwissProt_42:*  | 135    | 1      | MMGL_MOUSE  | P41300 mus musculu       |
| 27         | 138   | Scoring table: BLOSUM62  | 135    | 1      | V00B_FOWPV  | P14370 fowlpox vir       |
| 28         | 138   | Gapop 10.0 , Gapext 0.5  | 134    | 1      | NKGE_PANTR  | Q95ni4 pan troglod       |
| 29         | 138   | Total number of hits satisfying chosen parameters:   | 301    | 1      | LECI_RAT    | P08290 rattus norvegicus |
| 30         | 137.5 | Minimum DB seq length: 0   | 134    | 1      | NKG_A_MACMU | Q9mz9 macaca mulu        |
| 31         | 133   | Maximum DB seq length: 2000000000  | 233    | 1      | LY75_HUMAN  | Q60449 homo sapien       |
| 32         | 133   | Post-processing: Maximum Match 100%  | 129    | 1      | LECI_MOUSE  | P07307 homo sapien       |
| 33         | 132   | Listing First 45 summaries   | 128    | 1      | PGCA_MOUSE  | P70194 mus musculu       |

## ALIGNMENTS

| RESULT 1 |  | SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3). |         |
|----------|--|---|---------|
| CD94     | MACMU  | STANDARD;                                 | PRT;    |
| ID       | CD94_MACMU   |   | 179 AA. |
| AC       | Q9mz9; Q9GK31; Q9MKZ7; Q9MKZ8;   |   |         |
| DT       | 2B-FEB-2003 (Rel. 41, Created)   |   |         |
| DT       | 2B-OCT-2003 (Rel. 41, Last sequence update)  |   |         |
| DE       | Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).   |   |         |
| DE       | KLRD1 OR CD94.   |   |         |
| GN       | Macaca mulatta (Rhesus macaque).   |   |         |
| RP       | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Ceropithecinae; Macaca.  |   |         |
| RX       | [1] NCBI_TaxID=9544;   |   |         |
| RN       | SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  |   |         |
| RX       | MEDLINE:20322487; PubMed:10866118;   |   |         |
| RA       | Labonte M.L., Levy D.B., Letvin N.L.;  |   |         |
| RT       | "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, KLRD1 OR CD94."   |   |         |
| RT       | [1] RN   |   |         |
| RT       | SEQUENCE FROM N.A. (ISOFORM 1).  |   |         |
| RT       | MEDLINE:2115386; PubMed:11261935;  |   |         |
| RA       | Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; RT "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua.";  |   |         |
| RT       | RL Immunogenetics 53:69-73 (2001).   |   |         |
| CC       | -1- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-B molecules by NK cells and some cytotoxic T-cells.  |   |         |
| CC       | -1- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family members.   |   |         |
| CC       | -1- SUBCELLULAR LOCATION: Type II membrane protein.  |   |         |
| CC       | -1- ALTERNATIVE PRODUCTS:  |   |         |
| CC       | Event=Alternative splicing; Named isoforms=3;  |   |         |
| CC       | Name=1; Synonyms=CD94-A;   |   |         |
| CC       | Isoid=Q9Mz9-1; Sequence=Displayed;   |   |         |
| CC       | Name=2; Synonyms=CD94-B;   |   |         |
| CC       | Isoid=Q9Mz9-2; Sequence=VSP_003055;  |   |         |
| CC       | Name=3; Synonyms=CD94 alt;   |   |         |
| CC       | Isoid=Q9Mz9-3; Sequence=VSP_003054;  |   |         |
| CC       | -1- TISSUE SPECIFICITY: Natural killer cells.  |   |         |
| CC       | -1- SIMILARITY: Contains 1 C-type lectin family domain.  |   |         |
| CC       | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch). |   |         |
| DR       | EMBL: AF190931; AAF74527.1; -  |   |         |
| DR       | EMBL: AF190932; AAF74528.1; -  |   |         |

Query Match 17.5%; Score 180.5; DB 1; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 6e-11; Gaps 7;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

SEQUENCE 179 AA: 20607 MW: 602.2B4494527F07 CRC64;  
 Qy 44 GLUTVILMSLNYQYRILCCGS-----KDSTCSHCPSCPBLWTRNGS 84  
 Db 14 GTGIIICISLMLTGLIKNSTKLTKSYEPATPGPNIELQKSDC-C-SCHERWTGTYRC 70  
 Qy 85 HCYXFMSMEKKDWNNSLKFCAKGSHLWLTFPDNQGVKLFGEVYIGQDFWIGLNRID--GN 141.  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 71 NCYFISSEPKTEWNTSREIFCASOSSLQLQNRDDELMSS--SQHFWYQSYSEETHAW 128  
 Qy 142 RWEQQGPALSRLITLNLI---QRCGAATHRG-LQASSCEVALQWICKKVL 187  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 129 LWENGSSAQLFPLPSFTFKPKNCIAYNSKGNALECECTENRYICKQL 178

Result 2  
 NK11\_MOUSE STANDARD; PRT; 227 AA.  
 ID NK11\_MOUSE  
 AC P27811;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Natural killer cell surface protein P1-2 (NKR-P1.7).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.  
 OX NCBI\_TAXID=10090;  
 RP SEQUENCE FROM N.A.  
 MEDLINE=91349596; PubMed=1880421;

RN Giorda R., Trucco M.;  
 "Mouse NKR-P1. A family of genes selectively coexpressed in adherent  
 lymphocyte-activated killer cells.",  
 J Immunol. 147:1701-1708(1991).

RN [2]  
 SEQUENCE FROM N.A.  
 MEDLINE=9201315B; PubMed=1680927;  
 Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M.,  
 Seaman W.E.;  
 "cDNA cloning of mouse NKR-P1 and genetic linkage with Ly-49,  
 Identification of a natural killer cell gene complex on mouse  
 chromosome 6.",

RL J. Immunol. 147:3229-3236(1991).  
 CC -|- FUNCTION: May function as signal-transmitting receptor.  
 CC -|- SUBUNIT: Homodimer; disulfide-linked.  
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -|- TISSUE SPECIFICITY: Natural killer cells.  
 CC -|- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; M77676; AAA39822.1; -.  
 DR EMBL; M77753; AAA39366.1; -.  
 DR PIR; A46467; A46467.  
 DR HSP; P22897; LEGG  
 DR MG1; MG1:107540; Kirby.  
 DR InterPro; IPR002353; AntifreezeII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c\_1.  
 DR PRINTS; PRO0356; ANTIFREEZEII.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C\_TYPE-LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00041; C\_TYPE-LECTIN\_2; 1.  
 DR Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 DR CYTOPLASMIC (POTENTIAL).  
 DR SIGNAL\_ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 DR EXTRACELLULAR (POTENTIAL).  
 DR C-TYPE LECTIN (LONG FORM).  
 DR BY SIMILARITY.  
 DR 61 72  
 DR DISULFID 89 174  
 DR DISULFID 152 166  
 DR CARBOHYD 83 83  
 DR CARBOHYD 132 132  
 DR VARSPIC 1 34  
 DR MAVKTKTLWRLISGTGIIICUSLMTAGILKNS->MAA  
 (In isoform 3)  
 /FTId=ISP\_003054  
 /FTId=ISP\_003055  
 FT VARIANT 139 139 Y->D.  
 SQ 179 AA: 20607 MW: 602.2B4494527F07 CRC64;

Query Match 17.5%; Score 180.5; DB 1; Length 227;  
 Best Local Similarity 26.7%; Pred. No. 7.e-11; Gaps 31; Gaps 8;  
 Matches 58; Conservative 33; Mismatches 95; Indels 31; Gaps 8;

Qy 1 MADSSIXYSTELPEAPQVQDESRLWKL--KAVLHRPHLSRFAMVALGLL---TVILMSL 53  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 1 MDTARYFGLKXPRTPGAWHESPPSLPPDACPGRSPRSRALKLSCAGLILVVTLGMSV 60  
 Qy 54 LMQRILC-----CG-----SKDSTSCHCPSCPSPILWTPNHSKYYFSMKEKDWNSS 99  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 61 LV--RVLIQPKSIEKCYLVQENLNKTCDSAKLECPQDWLSHRDCKFHVSOVSNTWEG 118  
 Qy 100 LKFCADKGSHLTFPDNQGVLFGEYLQDF--YWIGLRLN--DGRWRWEGGPALS--L 151  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 119 LVDGDKGATMLIQDDBELFLIDSIKEKINSFWGLRTLPDMNKWKGTSNLSDVL 178  
 Qy 152 RILTNSLIQRGCAIHRNGLQASSCEVALQWICKVLY 188  
 :||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 179 KITGDITENDSCAAISGDKVTFESCNSDNRWICQKELY 215

RESULT 3  
 CD94\_HUMAN  
 ID CD94\_HUMAN STANDARD; PRT; 179 AA.  
 AC Q13241; O43321; Q9UEB3; Q9UEQ0;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Natural killer cells antigen CD94 (NK cell receptor)  
 DE lectin-like receptor subfamily D, member 1 (KP43).  
 DE Killer cell  
 GN KLRD1 OR CD94.



|            |   |                  |   |
|------------|---|------------------|---|
| DB         | lectin-like receptor subfamily D, member 1).                        | Qy               | 44 GILTVILMLMYQRILLCCGS-----KDISTCSHCPSCBILWTRNGS 84                    |
| GN         | KLRD1 OR CD94.  | Db               | 14 GTGIGIICLIS-MATLGILKNSFTKL-SIEPAFTPGPNTELQDSDC--C-SQEKNVGYRC 70      |
| CS         | Pan troglodytes (Chimpanzee).                                       | Qy               | 85 HCYFFSMEEKDNNSILKFCADKGSHLTFPDNQGYKLFGEYQDFYWIHLRNID--GW 141         |
| OC         | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   | Db               | 71 NCYFISSEQKTWNESRHLCAQSQQSSILQLONTDELFMSS---SQQPYWIGLSSSEHTAW 128     |
| CC         | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.           | Qy               | 142 RWEGGPALSRLTILTSLI---QRCGAHNRG-LOASSCEVALOWICKKV 187                |
| NCBI_TAXID | [1]   | Db               | 129 LWNGSALSQYTLFPSPETNDPKNCIAYNPNGNALDESCDKRYICKQL 178                 |
| OX         | SEQUENCE FROM N.A. (ISOFORM 1).                                     | Qy               |   |
| RP         | MEDLINE=20150666; PubMed=10894168;                                  | Db               |   |
| RA         | Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,    | Qy               |   |
| RA         | Muir D.G., Canavez F., Copper S.L., Vallante N.M., Lanier L.L.,     | Db               |   |
| RA         | Parham P.   | Qy               |   |
| RT         | "Rapid evolution of NK cell receptor systems demonstrated by        | Db               |   |
| RL         | comparison of chimpanzees and humans.";                             | Qy               |   |
| NN         | RL Immunity 12:687-698 (2000).                                      | Db               |   |
| NN         | [2]   | Qy               |   |
| RP         | ALTERNATIVE SPlicing.   | Db               |   |
| RX         | MEDLINE=211623889; PubMed=11751968;                                 | AC               | CD69_HUMAN STANDARD; PRT; 199 AA.                                       |
| RA         | Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I.,      | DT               | Q07108;   |
| RA         | Cleland S., Guehlein L.A., Unberg M., Parham P.;                    | DT               | 01-OCT-1994 (Rel. 30, Created)  |
| RT         | "Conservation and variation in human and common chimpanzee CD94 and | DT               | 01-OCT-1994 (Rel. 30, Last sequence update)                             |
| RT         | NKG2 genes."  | DT               | 15-MAR-2004 (Rel. 43, Last annotation update)                           |
| RT         | J. Immunol. 168:240-252 (2002).                                     | DE               | Early activation antigen CD69 (Early T-cell activation antigen p60)     |
| RL         | -!- FUNCTION: Plays a role as a receptor for the recognition of MHC | DE               | (GP32/28) (Leu-23) (MLR-3) (EA1) (BL-AC/P26) (Activation inducer        |
| CC         | CLASS I HLA-B molecules by NK cells and some cytotoxic T-cells.     | DB               | molecule) (AIM).  |
| CC         | -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family | GN               | CD69.   |
| CC         | members.  | OS               | Homo sapiens (Human).   |
| CC         | -!- SUBCELLULAR LOCATION: Type II membrane protein.                 | OC               | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.              |
| CC         | -!- ALTERNATIVE PRODUCTS:   | OC               |   |
| CC         | CC  | NCBI_TAXID=9606; |   |
| CC         | Event=Alternative splicing; Named isoforms=2;                       | RN               |   |
| CC         | Comment=Additional isoforms seem to exist;                          | RP               | SEQUENCE FROM N.A.  |
| CC         | Name=1; Synonyms=CD94 A;  | RC               | TISSUE=Blood;   |
| CC         | Isoid=Q9W41-1; Sequence-Displayed:                                  | RX               | Medline=93167093; PubMed=8496594;                                       |
| CC         | Name=2; Synonyms=CD94 B;  | RA               | Hamann J., Fiebig H., St-Sauss M.,                                      |
| CC         | Isoid=Q9W41-2; Sequence=VSP 003056;                                 | RT               | "Expression cloning of the early activation antigen CD69, a type II     |
| CC         | -!- TISSUE SPECIFICITY: Natural killer cells.                       | RT               | expression cloning of a C-type lectin domain."                          |
| CC         | -!- SIMILARITY: Contains 1 C-type lectin family domain.             | RL               | J. Immunol. 150:4920-4927(1993).  |
| CC         | -!- DOMAIN: Type II membrane protein.                               | RN               | [2]   |
| CC         | CC  | RP               | SEQUENCE FROM N.A., AND SEQUENCE OF 96-103; 128-146 AND 189-199.        |
| CC         | CC  | RC               | TISSUE=Blood;   |
| CC         | CC  | RX               | Medline=93340630; PubMed=8340578;                                       |
| CC         | CC  | RA               | Lopez-Cabreria M., Fernandez-Ruiz E., Blacher R.,                       |
| CC         | CC  | RA               | Santis A.G., Esch F., Sanchez-Madrid F., Armitage R.J.,                 |
| CC         | CC  | RA               | Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,                |
| CC         | CC  | RA               | Grobstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,     |
| CC         | CC  | RA               | Alderson M.R., Lopez-Cabreria M., Hamann J., Sanchez-Madrid F.,         |
| CC         | CC  | RT               | "Molecular cloning, expression, and chromosomal localization of the     |
| CC         | CC  | RT               | human earliest lymphocyte activation antigen AIM/CD69, a new member     |
| CC         | CC  | RT               | of the C-type animal lectin superfamily of signal-transmitting          |
| CC         | CC  | RT               | receptors."   |
| CC         | CC  | RL               | J. Immunol. 153:1643-1648(1993).  |
| CC         | CC  | RN               | [3]   |
| CC         | CC  | RP               | SEQUENCE FROM N.A.  |
| CC         | CC  | RX               | Medline=93314711; PubMed=8100776;                                       |
| CC         | CC  | RA               | Santis A., Lopez-Cabreria M., Sanchez-Madrid F., Armitage R.J.,         |
| CC         | CC  | RA               | Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,                |
| CC         | CC  | RA               | Grobstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,     |
| CC         | CC  | RA               | Alderson M.R., Lopez-Cabreria M., Hamann J., Sanchez-Madrid F.,         |
| CC         | CC  | RT               | "Structure of the gene coding for the human early lymphocyte            |
| CC         | CC  | RT               | activation antigen CD69: a C-type lectin receptor evolutionarily        |
| CC         | CC  | RT               | related with the gene families of natural killer cell-specific          |
| CC         | CC  | RT               | receptors,"   |
| CC         | CC  | RL               | Bur. J. Immunol. 23:1643-1648(1993).                                    |
| CC         | CC  | RN               | [4]   |
| CC         | CC  | RP               | SEQUENCE FROM N.A.  |
| CC         | CC  | RC               | Medline=94298875; PubMed=80265229;                                      |
| CC         | CC  | RA               | Santis A., Lopez-Cabreria M., Hamann J., Strauss M., Sanchez-Madrid F., |
| CC         | CC  | RA               | Grobstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,     |
| CC         | CC  | RA               | Alderson M.R., Lopez-Cabreria M., Hamann J., Sanchez-Madrid F.,         |
| CC         | CC  | RT               | "Molecular characterization of the early activation antigen CD69: a     |
| CC         | CC  | RT               | type II membrane glycoprotein related to a family of natural killer     |
| CC         | CC  | RT               | cell activation receptors."   |
| CC         | CC  | RL               | Bur. J. Immunol. 23:1643-1648(1993).                                    |
| CC         | CC  | RN               | [5]   |
| CC         | CC  | RP               | SEQUENCE FROM N.A.  |
| CC         | CC  | RC               | Medline=22388257; PubMed=12477932;                                      |
| CC         | CC  | RA               | Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  |
| CC         | CC  | RA               | Klaushner R.D., Collins F.S., Wagner L., Shevmen C.M., Schuler G.D.,    |
| FT         | FT  | FT               | Query Match Score 17.8%; Length 179;                                    |
| FT         | FT  | FT               | Best Local Similarity 31.8%; Prcd. No. 9.5e-11;                         |
| FT         | FT  | FT               | Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;          |







|  |         |  |  |
|--|---------|--|--|
| FT DOMAIN  | 1       | 70   | CYTOSMATIC (POTENTIAL).                  |
| FT TRANSMEM  | 71      | 93   | SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) |
| FT DOMAIN  | 94      | 233  | (POTENTIAL).                             |
| FT DOMAIN  | 118     | 231  | EXTRACELLULAR (POTENTIAL).               |
| FT DISULFID  | 119     | 130  | C-TYPE LECTIN (LONG FORM).               |
| FT DISULFID  | 147     | 229  | BY SIMILARITY.                           |
| FT DISULFID  | 208     | 221  | BY SIMILARITY.                           |
| FT CARBOHYD  | 102     | 102  | N-LINKED (GLCNAC, . .) (POTENTIAL).      |
| FT CARBOHYD  | 103     | 103  | N-LINKED (GLCNAC, . .) (POTENTIAL).      |
| FT CARBOHYD  | 180     | 180  | N-LINKED (GLCNAC, . .) (POTENTIAL).      |
| FT VARSPLIC  | 96      | 113  | Missing (in isoform NKG2-B).             |
| FT VARSPLIC  |         |  | /FTID=ySP 003066.                        |
| FT VARIANT   | 79      | 79   | I -> L (in NKG2-A*03).                   |
| FT VARIANT   | 231     | 231  | H -> R (in NKG2-A*03).                   |
| SQ SEQUENCE  | 233 AA; | 26212 MW;  | AE94BBA3A020984 CRC64;                   |
| Query Match  | 7       | YSTLELPAPQVODESRWKLKAVLHPRPHLSRFAMVALGGLTIVLM-----SLIM 55          |  |
| Best Local Similarity  | 15.4%   | Score: 158;  | DB 1; Length 233;                        |
| Best Local Similarity  | 23.5%   | Prod. No. 1.4e-08;   |  |
| Matches  | 46;     | Mismatches   | 29;                                      |
| Matches  | 29;     | Indels   | 36;                                      |
| Matches  | 29;     | Gaps   | 6;                                       |
| Qy   | 59      | YHCKDLPAPE-----KLVIGIIGIICUMLASWTVTIVIPSTLIQ 99                    |  |
| Db   | 56      | YQRILLCCGSKDSTCSHCPCSPCLILWTRNGSHCYYSMEKKDWNSLKECADKGSHLHLTFPD 115 |  |
| Qy   | 100     | RHNNSLSNTRTQRKARHCPCPEWWTYNSNCYYTIGERRTWESLSLACTSKNSGLSIDN 159     |  |
| Db   | 116     | NQGTKLFGFLGGDFWYGL-RNIDGWWE--GGPAASLRLLTINSLLQ-RCCAIHNGLQ 171      |  |
| Qy   | 160     | EEMKFLS--IISPSWIGVFRNSSSHFWVTINGLAFKHEIXDSDDNAELNCAVLQNGLK 217     |  |
| Db   | 172     | ASSCEVALQWICKRVL 187   |  |
| Qy   | 218     | SAQCGSSITIYHCKRKL 233  |  |
| RESULT 10  |         |  |  |
| IXB _ TRIFL  |         |  |  |
| ID _ IXB TRIFL   |         | STANDARD;  | PRT;                                     |
| AC P23807; Q91247;   |         |  | 146 AA.                                  |
| DT 01-NOV-1991 (Rel. 20, Created)  |         |  |  |
| DT 15-JUL-1998 (Rel. 36, Last sequence update)   |         |  |  |
| DT 10-OCT-2003 (Rel. 42, Last annotation update)   |         |  |  |
| DE Coagulation factor IX-binding protein B chain precursor (IX/X-BP).  |         |  |  |
| DE Trimeresurus flavoviridis (habu).   |         |  |  |
| OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |         |  |  |
| OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;   |         |  |  |
| OC Viperidae; Crotalinae; Trimeresurus.  |         |  |  |
| OX NCBI_TaxID=88087;   |         |  |  |
| RN [1]   |         |  |  |
| RP SEQUENCE FROM N.A.  |         |  |  |
| RX MEDLINE=96184662; PubMed=8645314;   |         |  |  |
| RX MEDLINE=91332000; PubMed=1831197;   |         |  |  |
| RA Atoda H., Ryoga M., Morita T.;  |         |  |  |
| RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;   |         |  |  |
| RT "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E."; |         |  |  |
| RT Biochem. Biophys. Res. Commun. 220:382-387(1996).   |         |  |  |
| RL [2]   |         |  |  |
| RN SEQUENCE OF 24-146.   |         |  |  |
| RC TISSUE-Venom;   |         |  |  |
| RX   |         |  |  |
| RA Atoda H., Ryoga M., Morita T.;  |         |  |  |
| RA "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E."; |         |  |  |
| RT Biochem. Biophys. Res. Commun. 220:382-387(1996).   |         |  |  |
| RL J. Biol. Chem. 266:14903-14911(1991).   |         |  |  |
| RN [3]   |         |  |  |
| RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  |         |  |  |
| RX MEDLINE=9733117; PubMed=9187649;  |         |  |  |

105 AAMLRYKAWAEESSCVYFKSTNNKWRSACRMMAQFVCE 143

-!- SUBCELLULAR LOCATION: Type II membrane protein.  
-!- ALTERNATIVE PRODUCTS:

| SULT 11<br>AA_HUMAN   | HUMAN<br>P26715; | STANDARD;<br>01 AUG-1992<br>01-AUG-1992<br>10-OCT-2003<br>NKCG2-A/NKG2-B | PRT;<br>Rel. 23, Created<br>Rel. 23, Last sequence update<br>(Rel. 42, Last annotation update)<br>Type II integral membrane protein<br>(NK cell receptor A). | 233 AA.<br>KLRC1 OR NKG2A.      |
|---|------------------|--|--|---------------------------------|
| <i> Homo sapiens (Human)</i><br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; <i> Homo sapiens</i> ; <i> Homo</i> |                  |  |  | NKG2A<br>NCBI_TaxID=606;<br>111 |

|  |
|--|
| -!- SUBCELLULAR LOCATION: Type II membrane protein.  |
| -!- ALTERNATIVE PRODUCTS:  |
| CC Event-Alternative splicing; Named isoforms=2;   |
| CC IsoId=P6715-1; Sequence=Displayed;  |
| CC Name=NKG2-A;  |
| CC IsoId=P6715-2; Sequence=VSP 003062;   |
| CC TISSUE SPECIFICITY: Natural killer cells.   |
| CC -!- SIMILARITY: Contains 1 C-type lectin family domain.   |
| CC   |
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| CC or send an email to license@isb-sib.ch).  |
| CC   |
| DR EMBL; X54867; CAA38649_1; -;  |
| DR EMBL; X54868; CAA38650_1; -;  |
| DR EMBL; UAB17133_1; -;  |
| DR EMBL; U54783; AAB17133_1; JOINED.   |
| DR EMBL; U54784; AAB17133_1; JOINED.   |
| DR EMBL; U54785; AAB17133_1; JOINED.   |
| DR AF023840; AAC17488_1; -;  |
| DR AF461812; AAI65234_1; -;  |
| DR BC012551; AAH12550_1; -;  |
| DR BC053840; AAH53840_1; -;  |
| DR PIR; PT0372; PT0372.  |
| DR HGNC; 6374; KLRC1.  |
| DR MIM; 161555; -;   |
| DR GO; 0005887; C:integral to plasma membrane; TAS.  |
| DR GO; 0004885; Transmembrane receptor activity; TAS.  |
| DR GO; 0006966; Plantimicrobial humoral response (senescent); TAS.   |
| DR GO; 0007166; Protein surface receptor linked signal transdu.  |
| DR InterPro; IPR01304; Lectin_C.   |
| DR Pfam; PF00059; lectin_c_1.  |
| DR SMART; SM00034; CHACT_1.  |
| DR PROSITE; PS00015; C_TYPELECTIN_1; FALSE_NEG.  |
| DR PROSITE; PS50041; C_TYPELECTIN_2; 1.  |
| KW Receptor; Transmembrane_Multigene Family; Signal-anchor; Lectin;  |
| KW Glycoprotein; Alternative splicing.   |
| FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).  |
| FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  |
| FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).  |
| FT DOMAIN 118 231 C-TYPE LECTIN (LONG FORM).   |
| FT DISULFID 119 130 BY SIMILARITY.   |
| FT DISULFID 147 229 BY SIMILARITY.   |
| FT DISULFID 208 221 BY SIMILARITY.   |
| FT CARBOHYD 102 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| FT VARSPlic 96 113 Missing (in isoform NKG2-B).  |
| FT FTid=VSP_003062;  |
| SQ SEQUENCE 233 AA; 26237 MW; 1654BD7958CB8A84 CRC64;  |
| Query Match 14.7%; Score 151; DB 1; Length 233;  |
| Best Local Similarity 23.0%; Pred. No. 7.2e-08;  |
| Matches 45; Conservative 29; Mismatches 86; Indels 36; Gaps 6  |
| Qy 7 YSTLELPPEAQVQDPSRWSRKLKAVIHLRPHLRFAMVALGLITLM-----SLLM 55   |
| Db 59 YHCKDLPSSA-----KLIVGIGICLILMASVTVVIVSTLIQ 99   |
| Qy 56 YCRILCCGSKDSTCSCPCPILWTRNGSHCYFSMEKKDWNSSLKFCADKGSHLTFPD 115   |
| Db 100 RHNSSLNTRTQRKARHCHGCPCEEWNTYSNSCCYIGKERRWEESTLACTSKNSLISDN 159  |
| Qy 116 NQGYKLGFGYLGDFYIIGI-RNIDGWRW -EGGEALSRLITLNLIQ-RGAIRHNLQ 171  |
| Db 160 FEPMFELS-TTSDPSWCAVERNSSPHDTYMTNGCFKPKVLYNDNATCQVNVVQV 217  |



|  |  |  |  |
|--|--|--|--|
| Best Local Similarity  | 22.8%  | Pred. No.  | 1.1e-07;   |
| Matches  | 49; Conservative   | 36; Mismatches   | 90; Indels   |
| Gap  | 8;   | Gaps   | 40;  |
| Score  | 5.6  | Score  | 5.6  |
| Y SITE LEPAQVOADES-----RWKLKAVLHPRHLSRFAWMALGLTILVMSL  | 53   | Y VADLNLRQEPKHDSPPSLSPDTCRPW-  | 59   |
| 54 LM-----YORILCQGSKDST-----CSHCPSCPILWTRNGSHCYYSFSMEKKDWNSSL  | 100  | 55 HRAL-KFGCAGLILLVUVGJ  | 59   |
| 60 CVLVLSVQKSVQKCAD/QENRHTTDSVNLEPQDWLSHRDCCFRFEQVSNTWEHQ  | 119  | 61 HRLA  | 59   |
| 101 KFCADKGSHLITFPDNOGYKLFGEVLYQDFE-YWIGRLN--DGMRMGGPALS--LR   | 152  | 102 ADCGRKGATULLIQQEEFLRLLDSIKECNFWIGLRFPLPDNNWNKNTGTTFNSDVK   | 179  |
| 153 ILTNSLILQRGCAIHNRGLQASSCEVALQWTCKKVL   | 187  | 154 ITGDIENGSCASISGDKVTSSESCSTDNRWICQKEL   | 214  |
| 180 ITGDIENGSCASISGDKVTSSESCSTDNRWICQKEL   | 214  |  |  |
| RESULT 14  |  |  |  |
| NKGD_MACMU   | STANDARD;  | PRT;   | 216 AA.  |
| ID NKGD_MACMU  | STANDARD;  | PRT;   | 216 AA.  |
| AC Q9MZU7;   | (Rel. 41, Created)   | DT 28-FEB-2003   | (Rel. 41, Last sequence update)  |
| DT 28-FEB-2003   | (Rel. 41, Last annotation update)  | DE NKG2-D type II integral membrane protein (NKG2-D activating NK receptor) (NK cell receptor D).  | GN NKG2D.  |
| OS Macaca mulatta (Rhesus macaque).  |  | RA Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.   | RA   |
| OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.   |  | OS Homo sapiens (Human).   | RA   |
| OX NCBI_TaxID=9544;  |  | OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.   | RA   |
| RN [1]   |  | OX NCBI_TaxID=9606;  | RA   |
| RP SEQUENCE FROM N.A.  |  | RN   | RP SEQUENCE FROM N.A.  |
| RA LaRonte M.L., Levy D.R., Letvin N.I.;   | "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D." | RA von Hoegen I., Nakayama E., Parnes J.R.;  | RA MEDLINE=90278102; PubMed=2141045;   |
| RT Immunogenetics 51:496-499 (2000).   |  | RT "Identification of a human protein homologous to the mouse Lyb-2 B cell differentiation antigen and sequence of the corresponding cDNA.";               | RA MEDLINE=92388257; PubMed=12477932;  |
| RL -   | -  | RT   | RA Klausner R.D., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Schaefer C.F., Blat N.K., Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Strelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C., Hara S.S., Loquellano N.A., Peters G.J., Green R.D., Dickson M.C., Bosak S.A., McEwan P.J., McKernan K.J.A., Malek J.A., Gunnarne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A., Falvey J., Heiton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E., Schein J.E., Jones S.J.M., Marrs M.A.; |
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| CC EMBL; AFI19043; AAP74539; -   |  | RA RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).   | RA RT  |
| DR InterPro; IPR001304; Lectin_C_  |  | CC - FUNCTION: Plays a role in B cell proliferation and differentiation. Associates with CDS.  | RA RT  |
| DR Pfam; PF00059; Lectin_C_1.  |  | CC - SUBUNIT: Homodimer; disulfide-linked.   | RA RT  |
| DR SMART; SM00034; CBCT_1.   |  | CC - SUBCELLULAR LOCATION: Type II membrane protein.   | RA RT  |
| DR PROSITE; PS50041; C_TYPELECTIN_1.   |  | CC - TISSUE SPECIFICITY: Pre-B-cells and B-cells but not terminally  | RA RT  |
| KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; KW Glycoprotein; Polymorphism.  | CYTOSMIC (POTENTIAL).  |  |  |
| FT DOMAIN 1 51   | SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  |  |  |
| FT TRANSMEM 52 72  | POTENTIAL).  |  |  |
| FT DOMAIN 73 216   | EXTRACELLULAR (POTENTIAL).   |  |  |
| FT DOMAIN 98 213   | C-TYPE LECTIN (LONG FORM).   |  |  |
| FT DISULFID 99 110   | BY SIMILARITY.   |  |  |
| FT DISULFID 127 211  | BY SIMILARITY.   |  |  |
| FT DISULFID 189 203  | BY SIMILARITY.   |  |  |

differentiated plasma cells.  
 CC -|- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -|- DATABASE: NAME=PIR; NOTE=CD entry CD72 entry.  
 CC WWW="http://www.ncbi.nlm.nih.gov/prok/CD/CD72.htm".

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DR MS4992; AA36189; 1.  
 EMBL; BC030227; AAH30227; 1; -.  
 DR PIR; A43532; A43532.  
 DR Genew; HGNC;1696; CD72.  
 DR MIM; 107272; -.  
 DR GO; GO:0005102; F:receptor binding; TAS.  
 DR GO; GO:0007155; P:cell adhesion; TAS.  
 DR InterPro; IPR003304; Lectin\_C.  
 DR Pfam; PF00059; Lectin\_c\_1.  
 DR SMART; SM00034; CLECT1; 1.  
 DR PROSITE; PS00615; C\_TYPELECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS00041; C\_TYPELECTIN\_2; 1.  
 DR KW Signal-anchor; Transmembrane; Lectin; Glycoprotein.  
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 96 116 SIGNAL\_ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 117 359 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 232 352 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 233 244 BY SIMILARITY.  
 FT DISULFID 261 350 BY SIMILARITY.  
 FT DISULFID 325 342 BY SIMILARITY.  
 FT CARBONID 136 136 N-LINKED (GLCNAC 1- ) (POTENTIAL).  
 SQ 359 AA; 40220 MW; 87A52C028AC17E44 CRC64;  
 SQ

Query Match 14.3%; Score 147.5; DB 1; Length 359;  
 Best Local Similarity 27.3%; Pred. No. 2.6e-07;  
 Matches 38; Conservative 19; Mismatches 61; Indels 21; Gaps 6;  
 Qy 62 CGSKDSTPSHCPSCPPIWTRNGSHCYFSMERRKDWNNSLKF CADKGSHLLTF---PDNQ 117  
 Db 226 CGSAD-TC---CPGWMIMHQKSCFTISLTSKWQBSQKCETLSKLATFSEIVYQSH 279

Qy 118 GVKLFGEYL---GQDYWIGLRNIDWRWEGCPALSIRILTNSLICRGAGTHR-----G 169  
 Db 280 SYFLNSLPLNGSGNYYWTGLSNSNKWKLTD----FQRTTYAQSSSKMKVHKTKWWWT 336

Qy 170 IQASSCTVALQWICKRQLY 188  
 Db 337 LESESCRSSLIPYICEMPAF 355

Search completed: August 10, 2004, 16:17:00  
 Job time : 8.32035 secs

| GenCore version 5.1.6<br>Copyright (c) 1993 - 2004 Compugen Ltd. |   | 1 protein - protein search, using sw mode!   |  |  |  |  |  |  |  |  |  |
|--|---|--|--|--|--|--|--|--|--|--|--|
|  |   | August 10, 2004, 16:11:32 ; Search time 32.6089 Seconds<br>(without alignments)<br>1819.059 Million cell updates/sec |  |  |  |  |  |  |  |  |  |
|  |   | Total number of hits satisfying chosen parameters:   |  |  |  |  |  |  |  |  |  |
|  |   | 1017041 seqs, 315518202 residues   |  |  |  |  |  |  |  |  |  |
|  |   | Search parameters:   |  |  |  |  |  |  |  |  |  |
| target:  | US-09-811-367B-3  | Minimum DB seq length: 0<br>Maximum DB seq length: 20000000000   |  |  |  |  |  |  |  |  |  |
| target-processing:   | 1 MADSIIXSTLELPAPQVQD.....GLQASSCEVALQWICKKVLY 188  | Match 0%<br>Maximum Match 100%<br>Listing First 45 summaries   |  |  |  |  |  |  |  |  |  |
| scoring table:   | BLOSUM62  | Gapop 10.0 , Gapext 0.5  |  |  |  |  |  |  |  |  |  |
| searched:  | 1017041 seqs, 315518202 residues  | Q9nz52 hom sapien  |  |  |  |  |  |  |  |  |  |
| scoring table:   | SPTREMBL_25:*   | Q8spx0 sus scrofa  |  |  |  |  |  |  |  |  |  |
| target database :  | SPTREMBL_25:*   | Q8mj05 macaca fasciata   |  |  |  |  |  |  |  |  |  |
| target database :  | 1: SP_archaea:*   | Q8mj10 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 2: SP_bacteria:*  | Q8mj13 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 3: SE_fungi:*   | Q8mj19 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 4: SP_human:*   | Q8mj41 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 5: SP_invertebrate:*  | Q8mj45 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 6: SP_mammal:*  | Q8mj53 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 7: SP_mhc:*   | Q8mj55 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 8: SP_organelle:*   | Q8mj57 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 9: SP_phage:*   | Q8mj59 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 10: SP_plant:*  | Q8mj61 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 11: SP Rodent:*   | Q8mj63 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 12: SP_virus:*  | Q8mj65 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 13: SP_vertebrate:*   | Q8mj67 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 14: SP_unclassified:*   | Q8mj69 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 15: SP_rvirus:*   | Q8mj71 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 16: SP_bacteriap:*  | Q8mj73 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| target database :  | 17: SP_archeap:*  | Q8mj75 pongo pygmaeus  |  |  |  |  |  |  |  |  |  |
| RESULT 1   |   |  |  |  |  |  |  |  |  |  |  |
| target:  | Q88713 ID   | SEQUENCE FROM N.A.   |  |  |  |  |  |  |  |  |  |
| target:  | AC 088713;  | SEQUENCE FROM N.A.   |  |  |  |  |  |  |  |  |  |
| target:  | DT 01-NOV-1998 (TREMBLrel.)   | SEQUENCE FROM N.A.   |  |  |  |  |  |  |  |  |  |
| target:  | DT 01-AUG-1999 (TREMBLrel.)   | SEQUENCE UPDATE  |  |  |  |  |  |  |  |  |  |
| target:  | DT 01-OCT-2003 (TREMBLrel.)   | SEQUENCE UPDATE  |  |  |  |  |  |  |  |  |  |
| target:  | DE Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like type II transmembrane receptor expressed by natural killer cells.) | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | DE Like receptor G1).   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | GN KLRG1 OR MAFA (Mouse)  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | OS Mus musculus (Mouse)   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus          | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | OC NCBI TaxID=10090;  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RN [1]  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RP [2]  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA Blaser C./ Blaser C./  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 088713 ratmusnorvegicus  | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 064335 ratterorariusnorvegicus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 076133 homosapiens   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 096393 homosapiens   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 043198 homosapiens   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 090636 galusgallus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 091v25 musmusculus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054708 musmusculus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054107 musmusculus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 025942 musmusculus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 061973 musmusculus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 08mj05 macaca fasciata   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 08mj10 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 08mj13 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 08mj19 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 08mj45 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   | SEQUENCE OF 2-188 FROM N.A.  |  |  |  |  |  |  |  |  |  |
| target:  | RA 054855 pongopygmaeus   |  |  |  |  |  |  |  |  |  |  |

|  |   |   |  |
|--|---|---|--|
| DR   | GO; GO:0004872; F:receptor activity; IEA.                           | Qy  | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60     |
| DR   | GO; GO:0005229; F:sugar binding; IEA.                               | Db  | 1 MADNSIYSTLELPPEAPRQDSSRWKYKAVLHRPCVSYLMWALGLITVILMSLLYQRL 60         |
| DR   | InterPro; IPR001304; P: heterophilic cell adhesion; Lectin_C.       | Db  | 1 MADNSIYSTLELPPEAPRQDSSRWKYKAVLHRPCVSYLMWALGLITVILMSLLYQRL 60         |
| Pfam   | PF00059; Lectin_c_1.  | Qy  | 1 CCGSKDSTCSHCPSCPILWTRNGSHCYYESMEKDNNSSLKFCADKGSHLTFPDNQGVK 120       |
| SMART  | SM00034; CLECTN_1.  | Db  | 1 CCGSKGFMCSQCSRCPENLWMENGSHCYFSEMEKDNNSSLKFCAKGSHLTFPDNQGVN 120       |
| DR   | PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.                              | Qy  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| KW   | Lectin_Receptor;  | Db  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| SEQUENCE   | 188 AA; 21396 MW; 87633602EA134F1 CRC64;                            | Qy  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Qy   | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60  | Db  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Db   | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60  | Qy  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Qy   | 100.0%; Score 1029; Pred. No. 1.5e-99; Length 188;                  | Db  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Best Local Similarity  | 100.0%; Pred. No. 1.5e-99;  | Qy  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Matches 188; Conservative 0; Misnatches 0; Indels 0; Gaps 0; | Db  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180 |  |
| Qy   | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60  | Qy  | 181 WICKKVLY 187   |
| Db   | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60  | Db  | 181 WICKKVLY 187   |
| Qy   | 61 CGGSKDSTCSHCPSCPILWTRNGSHCYFSEMEKDNNSSLKFCADKGSHLTFPDNQGVK 120   | RESULT 3  |  |
| Db   | 61 CGGSKDSTCSHCPSCPILWTRNGSHCYFSEMEKDNNSSLKFCADKGSHLTFPDNQGVK 120   | ID  | 075613   |
| Qy   | 121 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180  | ID  | 075613   |
| Db   | 121 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180  | AC  | 075613;  |
| Qy   | 121 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180  | DT  | 01-NOV-1998 (TREMBLrel. 08, Created)                                   |
| Db   | 121 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180  | DT  | 01-OCT-2003 (TREMBLrel. 25, Last sequence update)                      |
| Qy   | 181 WICKKVLY 188  | DB  | 01-OCT-2003 (TREMBLrel. 25, Last annotation update)                    |
| Db   | 181 WICKKVLY 188  | GN  | ITIM-containing receptor MAFA-L.                                       |
| Qy   | 181 WICKKVLY 188  | OS  | Homo sapiens (Human).  |
| Db   | 181 WICKKVLY 188  | OC  | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |
| Qy   | 181 WICKKVLY 188  | OC  | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.             |
| Db   | 181 WICKKVLY 188  | OX  | NCBI_TAXID=9606;   |
| Qy   | 181 WICKKVLY 188  | RN  | [1]  |
| Db   | 181 WICKKVLY 188  | RP  | SEQUENCE FROM N.A.   |
| Qy   | 181 WICKKVLY 188  | RA  | Butcher S., Arney K.L., Cook G.P.,                                     |
| Db   | 181 WICKKVLY 188  | RT  | "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene |
| Qy   | 181 WICKKVLY 188  | RT  | "2FL antigen, the mouse homolog of the rat 'SI' is a lectin-like type  |
| Db   | 181 WICKKVLY 188  | RL  | IT transmembrane receptor expressed by natural killer cells.";         |
| Qy   | 181 WICKKVLY 188  | RN  | [2]  |
| Db   | 181 WICKKVLY 188  | RP  | SEQUENCE FROM N.A.   |
| Qy   | 181 WICKKVLY 188  | RX  | Medline=9907194; PubMed=9862378;                                       |
| Db   | 181 WICKKVLY 188  | RA  | Ranke T., Corral L., Vance R.E., Raulet D.H.,                          |
| Qy   | 181 WICKKVLY 188  | RT  | "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene |
| Db   | 181 WICKKVLY 188  | RT  | "2FL antigen, the mouse homolog of the rat 'SI' is a lectin-like type  |
| Qy   | 181 WICKKVLY 188  | RL  | IT transmembrane receptor expressed by natural killer cells.";         |
| Db   | 181 WICKKVLY 188  | RN  | [2]  |
| Qy   | 181 WICKKVLY 188  | DR  | EMLB; AF081675; AAC32200.1;  |
| Db   | 181 WICKKVLY 188  | DR  | DR; GO:000529; F:sugar binding; IEA.                                   |
| Qy   | 181 WICKKVLY 188  | DR  | InterPro; IPR001304; Lectin_C.   |
| Db   | 181 WICKKVLY 188  | DR  | Pfam; PF00059; lectin_c_1.   |
| Qy   | 181 WICKKVLY 188  | DR  | SMART; SM00134; CLECT;   |
| Db   | 181 WICKKVLY 188  | DR  | PROSITE; PS50041; C_TYPELECTIN_2;                                      |
| Qy   | 181 WICKKVLY 188  | SQ  | SEQUENCE 189 AA; 21205 MW; FA9023F152365GA8 CRC64;                     |
| Db   | 181 WICKKVLY 188  | Query Match   | 55.2%; Score 568.5; DB 4; Length 189;                                  |
| Qy   | 181 WICKKVLY 188  | Best Local Similarity   | 57.2%; Pred. No. 2.3e-51;  |
| Db   | 181 WICKKVLY 188  | Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;      |  |
| Qy   | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60  | Qy  | 1 MADSSIYSTLELPPEAPOVQDESRWKILKAVLHRPHLSRFAMVALGLITVILMSLLMYQRL 60     |
| Db   | 1 MADNSIYSTLELPPEAPRQDSSRWKYKAVLHRPCVSYLMWALGLITVILMSLLYQRL 60      | Db  | 1 MTDSVTSMLPATAQNDYGPQOKSSSRPSCSCLVALALGLITAVLILSLLYQWL 60             |
| Qy   | 1 CCGSKDSTCSHCPSCPILWTRNGSHCYFSEMEKDNNSSLKFCAKGSHLTFPDNQGVK 120     | Qy  | 1 CCGSKDSTCSHCPSCPILWTRNGSHCYFSEMEKDNNSSLKFCAKGSHLTFPDNQGVK 120        |
| Db   | 1 CCGSKGFMCSQCSRCPENLWMENGSHCYFSEMEKDNNSSLKFCAKGSHLTFPDNQGVN 120    | Db  | 1 CQGSNTSTCASPSCDRWNYKGHHCYFSYVEKDNNSLKFCAKGSHLTFPDNQGVK 120           |
| Qy   | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180 | Qy  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Db   | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180 | Db  | 1.21 LGFEYLGQDFYWI GLENIDGMRWEGGPALSRLITNSLIQRCGAIRNGLOSSCEVALQ 180    |
| Qy   | 180 QWIKCKRV 186  | Qy  | 180 QWIKCKRV 186   |
| Db   | 181 HWVKCKRV 187  | Db  | 181 HWVKCKRV 187   |

|   |              |      |         |   |
|---|--------------|------|---------|---|
| RESULT 4  |              |      |         |   |
| Q96E93  | PRELIMINARY; | PRT; | 195 AA. |   |
| ID Q96E93;  |              |      |         |   |
| AC  |              |      |         |   |
| DT 01-DBC-2001 (TREMBrel. 19, Created)  |              |      |         |   |
| DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)   |              |      |         |   |
| DE Similar to killer cell lectin-like receptor subfamily G, member 1.   |              |      |         |   |
| OS Homo sapiens (Human).  |              |      |         |   |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.   |              |      |         |   |
| NCBI_TaxID=3606;  |              |      |         |   |
| OX [1]  |              |      |         |   |
| RP SEQUENCE FROM N.A.;  |              |      |         |   |
| RC TISSUE=bone marrow;  |              |      |         |   |
| RA Strassberg R.; Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.   |              |      |         |   |
| DR Genew; HGNC-6380; KIRG1.   |              |      |         |   |
| DR GO:0004872; F: receptor activity; IEA.   |              |      |         |   |
| DR GO:0005529; F: sugar binding; IEA.   |              |      |         |   |
| DR GO:0007157; P:heterophilic cell adhesion; IEA.   |              |      |         |   |
| DR InterPro; IPR0134; Lectin, C.  |              |      |         |   |
| DR Pfam; PF00059; lectin_c; 1.  |              |      |         |   |
| DR SMART; SM00034; CLECT; 1.  |              |      |         |   |
| DR PROSITE; PS50041; C_TYPELECTIN_2; 1.   |              |      |         |   |
| XW Lectin; Receptor.  |              |      |         |   |
| SQ SEQUENCE 195 AA; 21831 MW; 178EE98E08EBC473 CRC64;   |              |      |         |   |
| Query Match Score 54.9%; Score 564.5%; DB 4; Length 195; Best Local Similarity 57.0%; Pred. No. 6.1e-51; Indels 1; Gaps 1; Matches 106; Conservative 25; Mismatches 51; Indels 1; Gaps 1; |              |      |         |   |
| QY 1 MAASSIYSTLELPAPQVQDESRSWKLKAVLHRPHLSRFAMVALGLITVILMSLIMYQRLI 60  |              |      |         | RESULT 6  |
| Db 1 MTDSVITYSMELPLPTAQANDYGPQQKSRRPSCSCLVAIALGLLTAVLLSVLYQWL 60  |              |      |         | Q90636 PRELIMINARY; PRT; 257 AA.  |
| QY 61 CGGSXKDSTSCHPCSCPILWTRNGSHCYFSMERMKDWNSSLKPCADKGSHLLTEPDNQGVK 120   |              |      |         | ID Q90636; PRELIMINARY; PRT; 257 AA.  |
| Db 61 CGQSNYSTCACPSCPDRMKYGHHCYZFVEEKDWNSLLEFLARDSHLLVITDQNEMS 120  |              |      |         | AC Q90636; PRELIMINARY; PRT; 257 AA.  |
| QY 121 LFGBYLGDGYWIGLRNTIDWRMEGGPAALSL-RILTNSLIQRCGAIHENGLOSSCEVAL 179  |              |      |         | DB 01-NOV-1996 (TREMBrel. 01, Created)  |
| Db 121 LLQVFLSEAFCWIGLRNNSGWREDGSPLNFSRISSSNSFVQTGAINKNGLQASSCEVPL 180  |              |      |         | DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)                                       |
| QY 180 QWICKK 185   |              |      |         | DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)                                     |
| Db 181 HWCKK 186  |              |      |         | GN 17.5 protein.  |
| RP SEQUENCE FROM N.A.   |              |      |         | OS Gallus gallus (Chicken).   |
| RC TISSUE=spleen; PMID=8119728;   |              |      |         | OC Gallus gallus (Chicken).   |
| RA Bernto A., Zoorob R., Aufriay C.; RT "linkage of a new member of the lectin supergene family to the chicken Mhc gens."; RT Immunogenetics 38:221-229 (1994).                           |              |      |         | OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; NCBI_TaxID=9031; |
| DR IMPLB; M8B072; AA048558; 1; DR PMID: 94164691; PubMed=8119728;   |              |      |         | OC Gallus gallus (Chicken).   |
| RT "linkage of a new member of the lectin supergene family to the chicken Mhc gens."; RT Immunogenetics 38:221-229 (1994).  |              |      |         | OC Gallus gallus (Chicken).   |
| DR InterPro; IPR01304; Lectin, C.   |              |      |         | OC Gallus gallus (Chicken).   |
| DR Pfam; PF00059; lectin_c; 1.  |              |      |         | OC Gallus gallus (Chicken).   |
| DR SMART; SM00034; CLECT; 1.  |              |      |         | OC Gallus gallus (Chicken).   |
| DR PROSITE; PS50041; C_TYPELECTIN_2; 1.   |              |      |         | OC Gallus gallus (Chicken).   |
| SQ SEQUENCE 257 AA; 28814 MW; G67EA483F4E85333 CRC64;   |              |      |         | OC Gallus gallus (Chicken).   |
| Query Match Score 17.7%; Score 182; DB 13; Length 257; Best Local Similarity 28.7%; Pred. No. 8.6e-11; Mismatches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;                  |              |      |         | OC Gallus gallus (Chicken).   |
| QY 32 RPHLSRFAMVALG---LITVILMSLIMYQRLICCGSKDSTCSHCPSCPILTRNGSHCY 87   |              |      |         | OC Gallus gallus (Chicken).   |
| RP SEQUENCE FROM N.A.   |              |      |         | OC Gallus gallus (Chicken).   |
| RC TISSUE=Lung;   |              |      |         | OC Gallus gallus (Chicken).   |
| RX MEDLINE=98438735; PubMed=9765598;  |              |      |         | OC Gallus gallus (Chicken).   |
| RA Lamers M.B., Lamont A.G., Williams D.H.; RT Human MFA has alternative spliced variants.';  |              |      |         | OC Gallus gallus (Chicken).   |
| RL Biochim Biophys Acta 1399:209-212(1998).   |              |      |         | OC Gallus gallus (Chicken).   |
| DR EMBL; AAC34952; AAC34731.1; -.   |              |      |         | OC Gallus gallus (Chicken).   |



STRAIN=CS7BL/6J;  
Heuer J.W.; Ho E.L.; Brown M.G.; Mattsumoto K.; Yokoyama W.M.;  
"Murine CD94,"; Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).  
RN [3]

SEQUENCE FROM N.A.

STRAIN=CS7BL/6J; TISSUE=Mammary gland;  
Butcher S., Cottage A., Cook G.P.; "Mouse natural killer cell receptors homologous to human CD94 and NK2-D," submitted (DEB-1997) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF030311; AAC28243; 1; -.  
DR EMBL; AF057714; AAC33713; 1; -.  
DR EMBL; AF030225; AAP02116; 1; -.  
DR MGD; MGI:1196275; Klrdb1  
GO; GO:005523; F:sugar binding; IEA.  
GO; GO:0007157; P:heterophilic cell adhesion; IEA.  
InterPro; IPR006209; EGF like.  
InterPro; IPR001004; Lectin\_C.  
Pfam; PS00059; lectin\_c; 1.  
SMART; SM00034; CLECT1.  
PROSITE; PS00041; C\_TYPELECTIN\_2; 1.  
PROSITE; PS00022; EGF\_1; 1.  
Lectin.  
SEQUENCE 179 AA; 20808 MW; DD343419E93B3465 CRC64;

Query Match 17.5%; Score 180; DB 11; Length 179;  
Best Local Similarity 31.8%; Pred. No. 9.2e-11;  
Matches 57; Conservative 25; Mismatches 75; Indels 22; Gaps 9;

QY 22 SRWKLKAVHLRPHLSREAAAVALGHLTIVLMSLYRITCCGSKDST---CSHCPCSCP 76  
Db 7 TRWRLMSVFLGIK-CLEMYVTLG--VLIINSFTQIPOSTPSPRTTIVFQEVSSECCVQI 62

QY 77 ILWTRNGSICYYFSMEKDNNSKRFCAKDGSHLITFPPNQYLGDFYIWIGH- 135  
Db 63 DKWYGHQNCYCFISKEEKWSKRSRDFCAQSNSLLQ-PSQRNLSEFNE-SQFFWIGH 120

QY 136 ---RNIDGWRWEGGPALSLRILTN-SIIRQGAI---HENGQLASSCEVALWICKY 186  
Db 121 YSEKRNN--AWLWEDGTVPSKRDLFPFESVTRPEHCVYSSPSKSVAESCIENKNYICKL 177

RESULT 1.0

Q935G4 PRELIMINARY; PRT; 227 AA.  
ID Q935G4  
AC Q935G4  
DT 01-DEC-2001 (TREMBrel. 19, Created)  
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
DE Natural killer cell receptor protein NKR-P1A.  
OS Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]

SEQUENCE FROM N.A.

STRAIN=S/J; MEDLINE=9248165; PubMed=10229823;  
Kung S.K.P.; Su R.C.; Shannon J.; Miller R.G.; "The NKR-P1B gene product is an inhibitory receptor on S/J NK cells." J. Immunol. 162:5876-5887(1999).  
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S/J;  
RA Kung S.K.P.; Su R.C.; Shannon J.; Miller R.G.; Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
EMBL; AF354261; ARK39101.1; -.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:005523; F:sugar binding; IEA.  
InterPro; IPR002333; AntifreezeII.  
InterPro; IPR001304; Lectin\_C.

DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT1.  
DR PROSITE; PS00041; C\_TYPELECTIN\_2; 1.

KW SEQUENCE 227 AA; 25756 MW; 7109A2417DF9CBF1 CRC64;

Query Match 17.4%; Score 179.5; DB 11; Length 227;  
Best Local Similarity 26.7%; Pred. No. 1.4e-10;  
Matches 58; Conservative 33; Mismatches 95; Indels 31; Gaps 8;

QY 1 MADSSIYSTLELPAPQVODESRWKLKAVLHR-PHLSRPM---VALGLLTIVLMSLIM 55  
Db 1 MDTARVYFGKPPPTGAWHESSPPSLPPDACRCPRSRHLALKLSCAGLILVLTIGMSV 60

56 YORILIC-----CG-----SxDSTCSHCPSCPILLWTRNGSICYYFSMEKDNNSLKL 101  
61 LVRVLIQKPSIEKYYVLIQENLNKTIDSAAKLEPQDWLISHRDCKFCFHSHVSNTWEKGIV 120

62 FCADKGSHLITFPDNQYKLFGELYLGDFE--YNTGLRNI--DGWRWEGGPALS--LRI 153  
121 DCDDGATMLQDQEEFRFLDSIKEYCNSFWPLGLRTLPDMNWKWTNGSTNSDVLRKI 180

154 LTNSLIQRGCAIRHNGLQASSCEVALQICKVLY 188  
Db 181 TDDTENDSCAAISDKVTFESCNSDNRWICOKELY 215

RESULT 1.1

Q61973 PRELIMINARY; PRT; 227 AA.  
ID Q61973  
AC Q61973  
DT 01-NOV-1996 (TREMBrel. 01, Created)  
DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)  
DR EMBL; X64716; CAA45971.1; JOINED.  
DR EMBL; X64717; CAA45971.1; JOINED.  
DR EMBL; X64718; CAA45971.1; JOINED.  
DR HSSP; P22897; LEGS.  
DR MGD; MGI:107540; Kirbla.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005329; F:sugar binding; IEA.  
DR InterPro; IPR002353; AntifreezeII.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; ANTIFREEZEII.  
DR PROSITE; PS00041; C\_TYPELECTIN\_2; 1.

KW SEQUENCE 227 AA; 25756 MW; 7109A2417DF9CBF1 CRC64;

Query Match 17.4%; Score 179.5; DB 11; Length 227;  
Best Local Similarity 26.7%; Pred. No. 1.4e-10;  
Matches 58; Conservative 33; Mismatches 95; Indels 31; Gaps 8;

QY 1 MADSSIYSTLELPAPQVODESRWKLKAVLHR---KAVLHRRPHLSRFAMVALGL---TVIIMSL 53  
Db 1 MDTARVYFGKPPPTGAWHESSPPSLPPDACRCPRSRHSALKLSCAGLILVLTIGMSV 60

|    |     |   |     |   |
|----|-----|---|-----|---|
| QY | 54  | I MYQRLIC-----CG-----SKDSTCSCPSCPILWTRNGSHCYFSMEKIDWNSS       | 99  | POPY-NKG2A.   |
| Db | 61  | I V-----RVLQIKSIEKCVLQIENLNKTDCAKLECDWLRDKFHVSHVSNTWEEG       | 118 | OS Pongo pygmaeus (Orangutan).  |
| QY | 100 | I KFCADKGSHLTFPQDQVKLGEFYIGDFP-YWIGLRNI--DCWRWEGGPALS--L      | 151 | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |
| Db | 119 | I VDCCDGKATMLQDQEELREFLDSKEKZNFWGLRYTLPDMMWKWINGSTNSDVL       | 178 | OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  |
| QY | 152 | RILTNSLIQRCCAIHRNGLQASSCEVFLQWICKKVLY                         | 188 | NCBI_TAXID=9600;  |
| Db | 179 | KITDDRENDSCAAISGIVKTPFESCNDRWICQKELY                          | 215 | RN SEQUENCE FROM N.A.   |
|    |     |   |     | RP MEDLINE=22072112; PubMed=12077248;   |
|    |     |   |     | RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;  |
|    |     |   |     | RT "NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";  |
|    |     |   |     | RT J. Immunol. 169:2220-2229 (2002).  |
|    |     |   |     | RL IMMUNOL; AF470395; AAC78495.1;   |
|    |     |   |     | DR GO; GO:0004872; F:sugar binding; IEA.  |
|    |     |   |     | DR GO; GO:0005529; F:sugar binding; IEA.  |
|    |     |   |     | DR GO; GO:0001157; F:heterophilic cell adhesion; IEA.   |
|    |     |   |     | DR InterPro; IPR001304; Lectin_C.   |
|    |     |   |     | DR Pfam; PF00059; lectin_c_1.   |
|    |     |   |     | DR SMART; SM00034; CLECT_1.   |
|    |     |   |     | DR PROSITE; PS50041; C_TYPE_LECTIN_2_1.   |
|    |     |   |     | KW Receptor; Lectin_SQ; Conservative_SQ; Mismatches_SQ; Indels_SQ; Gaps_SQ  |
|    |     |   |     | Query Match Score 177; DB 6; Length 233; Best Local Similarity 24.5%; Pred. No. 2.6e-10; Matches 48; Conservative 28; Mismatches 84; Indels 36; Gaps 6; |
| Qy | 7   | YSTLELPAPQVQDESRWKLKAVLHRPHLSRFAMYALGLLTIVLM-----SLIM         | 55  | Qy 7 YSTLELPAPQVQDESRWKLKAVLHRPHLSRFAMYALGLLTIVLM-----SLIM  |
| Db | 59  | YHCKDLPSAPE-----KLVIGLIGITCLVLMASVVTIVVIPSTLIQ                | 99  | Db 59 YHCKDLPSAPE-----KLVIGLIGITCLVLMASVVTIVVIPSTLIQ  |
| Qy | 56  | YQRILCGGSKDSTSCHSCPSCPILWTRNGSHCYFSMEKDNNSLKFCKGSHLTFPD       | 115 | Qy 56 YQRILCGGSKDSTSCHSCPSCPILWTRNGSHCYFSMEKDNNSLKFCKGSHLTFPD   |
| Db | 100 | KHNSSSLNTRTOKAHRCGHCPDEEWITYNSNCYIGKEKRTEWEILLACASKNSLLSDIN   | 159 | Db 100 KHNSSSLNTRTOKAHRCGHCPDEEWITYNSNCYIGKEKRTEWEILLACASKNSLLSDIN  |
| Qy | 116 | NQGVKLFGEYLQDFYIWGL-RNIDGWRE--GGPALSRLTNTSLIQR-CGAIRHNLQ      | 171 | Qy 116 NQGVKLFGEYLQDFYIWGL-RNIDGWRE--GGPALSRLTNTSLIQR-CGAIRHNLQ   |
| Db | 160 | EEEMKEFGTIIPLFS-S-WIGVRNSSHHPWTTINGLAFKQEQTKDSDNAEHDAVLTFRGLR | 217 | Db 160 EEEMKEFGTIIPLFS-S-WIGVRNSSHHPWTTINGLAFKQEQTKDSDNAEHDAVLTFRGLR  |
| Qy | 172 | ASCEVALQWICKKVLY  | 187 | Qy 172 ASCEVALQWICKKVLY   |
| Db | 218 | SNKGSSILYHCKHL  | 233 | Db 218 SNKGSSILYHCKHL   |
|    |     |   |     | RESULT 14   |
|    |     |   |     | Q95L94 PRELIMINARY; PRT; 236 AA.  |
|    |     |   |     | ID Q95L94 ID Q95L94 PRELIMINARY; PRT; 236 AA.   |
|    |     |   |     | AC Q95L94 AC Q95L94   |
|    |     |   |     | DT 01-DEC-2001 (TREMBLrel. 19, Created)   |
|    |     |   |     | DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  |
|    |     |   |     | DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  |
|    |     |   |     | GN NGK2-B3.   |
|    |     |   |     | OS Macaca mulatta (Rhesus macaque).   |
|    |     |   |     | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |
|    |     |   |     | OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;   |
|    |     |   |     | OC Cercopithecinae; Macaca.   |
|    |     |   |     | OX NCBI_TAXID=9544;   |
|    |     |   |     | RN [1] FROM N.A.  |
|    |     |   |     | RP LaBonte M.L., Letvin N.L.; Analysis of rhesus monkey CD94/NKG2 family members."  |
|    |     |   |     | RT Submitted (JUN-2001) to the ENBL/GenBank/DDBJ databases.   |
|    |     |   |     | DR EMBL; AF395617; AAC77464.1;  |
|    |     |   |     | DR GO; GO:000559; F:sugar binding; IEA.   |
|    |     |   |     | DR InterPro; IPR001304; Lectin_C.   |
|    |     |   |     | DR SMART; SM00034; CLECT_1.   |
|    |     |   |     | DR PROSITE; PS50041; C_TYPE_LECTIN_1.   |
|    |     |   |     | DR PROSITE; PS50041; C_TYPE_LECTIN_2.   |
|    |     |   |     | SQ SEQUENCE FROM N.A.   |
| QY | 44  | GLTVLWMLMQRILCCGS-----KDSTCSHCPSCPILWTRNGS                    | 84  | QY 44 GLTVLWMLMQRILCCGS-----KDSTCSHCPSCPILWTRNGS  |
| Db | 14  | GPIGIICLSLMATTGILKNSFTKLSIEPAFTP GDPDIELQKDSDC--C-SQCEKWNYGRC | 70  | Db 14 GPIGIICLSLMATTGILKNSFTKLSIEPAFTP GDPDIELQKDSDC--C-SQCEKWNYGRC   |
| Qy | 85  | HCYYFSMEKDWNSLXPKCADKGSHLTFPDNGQVLFQGEYLQDFWIGRNID--GW        | 141 | Qy 85 HCYYFSMEKDWNSLXPKCADKGSHLTFPDNGQVLFQGEYLQDFWIGRNID--GW  |
| Db | 71  | NCYFISSEQTKWNEFHICASQKSSLQNTDLDMS--SQQFTWIGLSSYSEBTAW         | 128 | Db 71 NCYFISSEQTKWNEFHICASQKSSLQNTDLDMS--SQQFTWIGLSSYSEBTAW   |
| Qy | 142 | RWEGGPALS---LRLTINSLIIORGCAIHRNG-LQASCEVALQWICKKVLY           | 187 | Qy 142 RWEGGPALS---LRLTINSLIIORGCAIHRNG-LQASCEVALQWICKKVLY  |
| Db | 129 | LWENGSAISQYLPETFNPKNCIAWPNGNALDESCDKNYICRQQ                   | 178 | Db 129 LWENGSAISQYLPETFNPKNCIAWPNGNALDESCDKNYICRQQ  |
|    |     |   |     | RESULT 13   |
|    |     |   |     | Q8MJH7 PRELIMINARY; PRT; 233 AA.  |
|    |     |   |     | AC Q8MJH7 AC Q8MJH7 PRELIMINARY; PRT; 233 AA.   |
|    |     |   |     | DT 01-OCT-2002 (TREMBLrel. 22, Created)   |
|    |     |   |     | DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  |
|    |     |   |     | DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  |
|    |     |   |     | DT Natural killer cell lectin-like receptor.  |

Query Match Similarity 17.2%; Score 177; DB 6; Length 236;  
 Best Local Similarity 25.0%; Pred. No. 2.6e-10;  
 Matches 47; Conservative 33; Mismatches 82; Indels 26; Gaps 7;

Db 139 CNPCKTQWYGNSSCYYSINBEKWSNSRKCDCIDRNATLWKIDSTEBRDILQLQSLSITP 198  
 Qy 20 DESRWKLKAVLHRPHLSRPAVGLLTUTLMSLLMYORIL--CCG-----S 64  
 DR 55 NDKTYHCKRLPPP--EKLTAEVIGIICIVLMAVTKVPLIPIGVNLQNNEFSLNTRIQ 112  
 Qy 65 KDSCTSHCSHCPSCPIUWTRNGSHCXXFSMEKKDWNNSLIKECADKSHILLFPDNQVKLFG 124  
 Db 113 KAYNGGHCPDEEWITYTN --CYTIGKERTWEELTCASKNSNLLSTDNEEEMOLIGS 169  
 Qy 125 YLGDDFYWGLRNIDG--WRWEGGPALSRLIRITNSL-LIQRCGAIRHNGLQASCEVAlQ 180  
 Db 170 L--SVLSWGVSRSSSDHPPWUSINGSTPKLKIAESDICRHNCTMHLSSQLSKSHRCGSQL 227  
 Qy 181. WICKKVLY 188  
 Db 228 YTCKXHKLW 235

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**RESULT 15**

Q94403 PRELIMINARY; PRT; 275 AA.  
 ID Q9D403  
 AC Q9D403;  
 DT 01-JUN-2001 (TREMBrel. 17, Created)  
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE 4933425B16Rik protein.  
 GN 4933425B16Rik  
 OS Mus musculus (Mouse).  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Testis;  
 RX MEDLINE=21085660; Pubmed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno H., Adachi J., Fukuda S.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shitara Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2000).  
 DR EMBL; AR016908; BAB30491.1;  
 DR HSSP; P23807; IIXX.  
 DR MGD; MG1:1918433; 4933425B16Rik.  
 DR GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 SQ SEQUENCE 275 AA, 313360 MW, C9792BA25CB85CC2 CRC64;

Query Match Similarity 17.2%; Score 177; DB 11; Length 275;  
 Best Local Similarity 31.7%; Pred. No. 3.1e-10;  
 Matches 40; Conservative 17; Mismatches 57; Indels 12; Gaps 5;

Qy 72 CPSPCILWTRNGSHCYYFSM-EKKDWNSSLFKFCADKGSHLLFPDNQGVKLFGEYLGQ- 128

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composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFa binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFa protein.

XX Sequence 188 AA;

Query Match 100.0%; Score 1029; DB 4; Length 188;  
Best Local Similarity 100.0%; Pred. No. 6.6e-103;  
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSSIVSTLEPAPQVQDESRWKLUKAVLRPHLSFPAVYALGLLTIVLMSLLMYQRIL 60  
Db 1 MADSSIVSTLEPAPQVQDESRWKLUKAVLRPHLSFPAVYALGLLTIVLMSLLMYQRIL 60

Qy 61 CGGSKDSTCSSHCPSCPILWTRNGSHCYFSMEEKKDWNNSLKFCA DKSHLITFPDNGVK 120  
Db 61 CGGSKDSTCSSHCPSCPILWTRNGSHCYFSMEEKKDWNNSLKFCA DKSHLITFPDNGVK 120

Qy 121 LFGEYLQDFYTGRLNIDGMRWE GGPA LSRLTNSLIQRGATIHRNGLQASCEVALQ 180  
Db 121 LFGEYLQDFYTGRLNIDGMRWE GGPA LSRLTNSLIQRGATIHRNGLQASCEVALQ 180

Qy 181 WICKKVLY 188  
Db 181 WICKKVLY 188

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RESULT 3  
AAW88277 ID AAW88277 standard; protein; 188 AA.  
XX AC AAW88277;  
XX DT 29-MAR-1999 (first entry)  
XX DE Rat mast cell function-associated antigen (MAFa).  
XX ID AAR77033 standard; protein; 188 AA.  
XX AC AAR77033;  
XX DT 01-FEB-1996 (first entry)  
XX DE Mammalian mast cell function-associated antigen (MAFa).  
XX KW Mast cell function-associated antigen; MAFa; soluble; ligand; inflammatory; screening; allergic; prevention.  
XX OS Rattus rattus.  
XX PN WO9527734-A1.  
XX PD 19-OCT-1995.  
XX PR 06-APR-1995; 95WO-US004258.  
XX PR 08-APR-1994; 94IL-00109257.  
XX PA (YEDA ) YEDA RES & DEV CO LTD.  
PA (RYCU/) RYCUS A.  
PI Pecht I, Guthmann MD, Tal M,  
DR WPI; 1995-366356/47.  
DR N-PSDB; AAT01471.

Novel DNA encoding a mast cell function-associated antigen (MAFa) - useful for screening for ligands of MAFa which are useful for prevention of inflammatory and allergic reactions.

Claim 12; Page 37; 54pp; English.

PT Novel DNA encoding a mast cell function-associated antigen (MAFa) - useful for screening for ligands of MAFa which are useful for prevention of inflammatory and allergic reactions.

PS Claim 12; Page 37; 54pp; English.

CC combination with the MAFa to prevent inflammatory and allergic reactions

XX XX Sequence 188 AA;

Query Match 81.4%; Score 838; DB 2; Length 188;  
Best Local Similarity 80.7%; Pred. No. 3.2e-82;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSIVSTLEPAPQVQDESRWKLUKAVLRPHLSFPAVYALGLLTIVLMSLLMYQRIL 60  
Db 1 MADSSIVSTLEPAPQVQDESRWKLUKAVLRPHLSFPAVYALGLLTIVLMSLLMYQRIL 60

Qy 61 CGGSKDSTCSSHCPSCPILWTRNGSHCYFSMEEKKDWNNSLKFCA DKSHLITFPDNGVK 120  
Db 61 CGGSKDSTCSSHCPSCPILWTRNGSHCYFSMEEKKDWNNSLKFCA DKSHLITFPDNGVK 120

Qy 121 LFGEYLQDFYTGRLNIDGMRWE GGPA LSRLTNSLIQRGATIHRNGLQASCEVALQ 180  
Db 121 LFGEYLQDFYTGRLNIDGMRWE GGPA LSRLTNSLIQRGATIHRNGLQASCEVALQ 180

Qy 181 WICKKVLY 187  
Db 181 WICKKVLY 187

---

RESULT 3  
AAW88277 ID AAW88277 standard; protein; 188 AA.  
XX AC AAW88277;  
XX DT 29-MAR-1999 (first entry)  
XX DE Rat mast cell function-associated antigen (MAFa).  
XX ID AAR77033 standard; protein; 188 AA.  
XX AC AAR77033;  
XX DT 01-FEB-1996 (first entry)  
XX DE Mammalian mast cell function-associated antigen (MAFa).  
XX KW Mast cell function-associated antigen; MAFa; splice variant; rat; inflammation; allergy; asthma; tumour; therapy.  
XX OS Rattus sp.  
XX PH Key Location/Qualifiers  
FT Modified-site 82..84  
FT /note= "Asn is N-glycosylated"  
FT Modified-site 97..99  
FT /note= "Asn is N-glycosylated"  
XX PN WC9854209-A2.  
XX PD 03-DEC-1998.  
XX PT 29-MAY-1998;  
XX PN 98WO-GB001572.  
XX PR 31-MAY-1997; 97GB-00011148.  
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  
XX DR WPI; 1999-059806/05.  
XX DR N-PSDB; AAV84222.  
XX PT New polypeptide having a sequence corresponding to human mast cell function-associated antigens - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  
XX Disclosure; Fig 4; 44pp; English.  
CC This is the amino acid sequence of rat mast cell function-associated antigen (MAFa), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFa molecule (see ARW88265) and to the discovery of splice variants (see AAW88266-67)  
CC of human MAFa that are not found in rat. Polypeptides and synthetic CC



The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a Promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.htm?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

|                       |  |
|-----------------------|--|
| DE                    | Partial sequence of mast cell function-associated antigen (MAFA).  |
| XX                    | Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergy; prevention.  |
| KW                    |  |
| KW                    |  |
| XX                    | Rattus ratus.  |
| XX                    | PN   |
| XX                    | WO9527734-A1 .   |
| XX                    | PD   |
| XX                    | 19-OCT-1995 .  |
| XX                    | PF   |
| XX                    | 06-APR-1995 ;  |
| XX                    | 95WO-US04258 .   |
| XX                    | PR   |
| XX                    | 08-APR-1994 ;  |
| XX                    | 94IL-00109257 .  |
| XX                    | PA   |
| XX                    | (YEDA ) YEDA, RES & DEV CO LTD .   |
| XX                    | PA   |
| XX                    | (RYCUU) RYCUS A.   |
| XX                    | PI   |
| XX                    | Pecht I, Gubermann MD, Tal M;  |
| XX                    | DR   |
| XX                    | WPI ; 1995-366356/47 .   |
| XX                    | DR-N-PSDB ; AAT01471 .   |
| XX                    | PT   |
| XX                    | Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions. |
| XX                    | PT   |
| XX                    | CC   |
| XX                    | PS   |
| XX                    | PS Disclosure; Page 38 : 54pp; English.  |
| XX                    | SQ   |
| XX                    | Sequence 114 AA;   |
| Query                 | 53.5% Score 551; DB 2; Length 114;   |
| Best Local Similarity | 84.1%; Pred. No. 1.9e-51;  |
| Matches               | 95; Conservative 9; Mismatches 9; Indels 0; Gaps   |
| Qy                    | 75 CPIIWTTRGSHCYFSMEKKDNNSLKEFCDKGSHLITFDDNQGVKLFGEVLYLGQDFEWIG 13   |
| Db                    | 1 CPNIFWMRNGSHCYFSMEKKDNNSLKEFCDKGSHLITFDDNQGVKLFGEVLYLGQDFEWIG 60   |
| Qy                    | 135 LRRNDGWRMEEGGPALSRLTTSLSLQRCGATHRNGIQASSCEVALONICRKVL 187  |
| Db                    | 61 LRRDGWRMEEGGPALSRLTTSLSLQRCGATHRNGIQASSCEVALONICRKVL 113  |
| RESULT 7              |  |
| ID                    | AAW88265 standard; protein; 189 AA.  |
| XX                    |  |
| AC                    | AAW88265;  |
| XX                    |  |
| XX                    | 29 MAR-1999 (First entry)  |
| DE                    | Human mast cell function-associated antigen (MAFA).  |
| XX                    |  |
| KW                    | Mast cell function-associated antigen; MAFA; splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.  |
| XX                    |  |
| OS                    | Homo sapiens.  |
| XX                    |  |
| FH                    | Key Location/Qualifiers  |
| FT                    | Peptide 7..10 /note= "ITIM motif"  |
| FT                    | Modified-site 65..67 /note= "Asn is N-glycosylated"  |
| FT                    | Modified-site 97..99 /note= "Asn is N-glycosylated"  |
| FT                    | Modified-site 137..139 /note= "Asn is N-glycosylated"  |

|   |  |  |  |   |
|---|--|--|--|---|
| PT  | Modified-site  | /note= "Asn is N-glycosylated"   | KW   | immunosuppressive; cytostatic.  |
| PT  |  | 150...152  | XX   |   |
| PT  |  | /note= "Asn is N-glycosylated"   | OS   |   |
| XX  | PN   | W09854209-A2.  | XX   | Homo sapiens.   |
| XX  | PD   | 03-DEC-1998.   | PN   | WO200170805-A2.   |
| XX  | PF   | 29-MAY-1998;   | XX   | 27-SEP-2001.  |
| XX  | PR   | 98WO-GB001572.   | XX   | 16-MAR-2001; 2001WO-US008596.   |
| XX  | PA   | 31-MAY-1997;   | XX   | 17-MAR-2000; 2000ITIS-0190716P.   |
| XX  | (PEPT-) PEPTIDE THERAPEUTICS LTD.  |  | XX   | (GENI-) GEMINI SCI INC.   |
| XX  | PI   | Hewitt EL, Lamers MBAC, Lamont A, Williams DH,                         | XX   | PA  |
| XX  | DR   | WPI; 1999-05906/05.  | XX   | Takahashi N, Miyayama T;  |
| XX  | DR   | DR N-PSDB; AAV84198.   | XX   | PI  |
| PT  | New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  | PS   | XX   | XX  |
| PT  | Disclosure; Fig 1; 4pp; English.   | XX   | XX   | The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA), a type II membrane glycoprotein, cDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277), having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2. Alternatively spliced forms (see AAW88266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth. |
| XX  | This is the amino acid sequence of human mast cell function-associated antigen (MAFA), a type II membrane glycoprotein, cDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277), having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2. Alternatively spliced forms (see AAW88266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth. | PS   | XX   | CC  |
| XX  | Sequence 189 AA;   | XX   | XX   | CC  |
| XX  | Query Match Score 548.5; DB 2; Length 189;   | XX   | XX   | CC  |
| Best Local Similarity 55.6%; Pred. No. 7e-51; Matches 26; Mismatches 56; Indels 1; Gaps 1;  | XX   | XX   | XX   | CC  |
| Matches 104; Conservative 26; Mis matches 56; Indels 1; Gaps 1;   | XX   | XX   | XX   | CC  |
| Query Match Score 548.5; DB 4; Length 189;  | XX   | XX   | XX   | CC  |
| Best Local Similarity 55.6%; Pred. No. 7e-51; Matches 104; Conservative 26; Mis matches 56; Indels 1; Gaps 1;                                       | XX   | XX   | XX   | CC  |
| 1 MADSSITYSTLEPAPQYQODESRWKLKAVLHRPHLSRFAVALGLLTVILMSLIMYORIL 60  | 1 MADSSITYSTLEPAPQYQODESRWKLKAVLHRPHLSRFAVALGLLTVILMSLIMYORIL 60   | 1 MADSSITYSTLEPAPQYQODESRWKLKAVLHRPHLSRFAVALGLLTVILMSLIMYORIL 60       | 1 MADSSITYSTLEPAPQYQODESRWKLKAVLHRPHLSRFAVALGLLTVILMSLIMYORIL 60       | 1 MADSSITYSTLEPAPQYQODESRWKLKAVLHRPHLSRFAVALGLLTVILMSLIMYORIL 60  |
| Db 1 MTDSVIYSMELPLTQAONDYGPQQSSSKPSCSCLVAILGLLTAVLLSVLYQWIL 60  | Db 1 MTDSVIYSMELPLTQAONDYGPQQSSSKPSCSCLVAILGLLTAVLLSVLYQWIL 60   | Db 1 MTDSVIYSMELPLTQAONDYGPQQSSSKPSCSCLVAILGLLTAVLLSVLYQWIL 60         | Db 1 MTDSVIYSMELPLTQAONDYGPQQSSSKPSCSCLVAILGLLTAVLLSVLYQWIL 60         | Db 1 MTDSVIYSMELPLTQAONDYGPQQSSSKPSCSCLVAILGLLTAVLLSVLYQWIL 60  |
| QY 61 CCGSKDSTSCHCPSCPILMTRNGSHCYYSFMSMEKKDWNSSLKFADKGSHLTFPDNQGVK 120  | QY 61 CCGSKDSTSCHCPSCPILMTRNGSHCYYSFMSMEKKDWNSSLKFADKGSHLTFPDNQGVK 120   | QY 61 CCGSKDSTSCHCPSCPILMTRNGSHCYYSFMSMEKKDWNSSLKFADKGSHLTFPDNQGVK 120 | QY 61 CCGSKDSTSCHCPSCPILMTRNGSHCYYSFMSMEKKDWNSSLKFADKGSHLTFPDNQGVK 120 | QY 61 CCGSKDSTSCHCPSCPILMTRNGSHCYYSFMSMEKKDWNSSLKFADKGSHLTFPDNQGVK 120  |
| Db 61 CGGNNYSTASCSPCPDRMKYGRHHCYYSVEEDDWNSLLEFLARDSHLVTIDNQMS 120   | Db 61 CGGNNYSTASCSPCPDRMKYGRHHCYYSVEEDDWNSLLEFLARDSHLVTIDNQMS 120  | Db 61 CGGNNYSTASCSPCPDRMKYGRHHCYYSVEEDDWNSLLEFLARDSHLVTIDNQMS 120      | Db 61 CGGNNYSTASCSPCPDRMKYGRHHCYYSVEEDDWNSLLEFLARDSHLVTIDNQMS 120      | Db 61 CGGNNYSTASCSPCPDRMKYGRHHCYYSVEEDDWNSLLEFLARDSHLVTIDNQMS 120   |
| QY 121 LFGEYLGGQFYWIGLRNTIGWRWEGGPALSL-RILTNSLIQRCAIHNRGLOASSCEVAL 179  | QY 121 LFGEYLGGQFYWIGLRNTIGWRWEGGPALSL-RILTNSLIQRCAIHNRGLOASSCEVAL 179   | QY 121 LFGEYLGGQFYWIGLRNTIGWRWEGGPALSL-RILTNSLIQRCAIHNRGLOASSCEVAL 179 | QY 121 LFGEYLGGQFYWIGLRNTIGWRWEGGPALSL-RILTNSLIQRCAIHNRGLOASSCEVAL 179 | QY 121 LFGEYLGGQFYWIGLRNTIGWRWEGGPALSL-RILTNSLIQRCAIHNRGLOASSCEVAL 179  |
| Db 121 LLQYFLSEFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINNQLQASSCEVPL 180   | Db 121 LLQYFLSEFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINNQLQASSCEVPL 180  | Db 121 LLQYFLSEFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINNQLQASSCEVPL 180    | Db 121 LLQYFLSEFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINNQLQASSCEVPL 180    | Db 121 LLQYFLSEFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINNQLQASSCEVPL 180   |
| QY 180 QWICKKV 186  | QY 180 QWICKKV 186   | QY 180 QWICKKV 186   | QY 180 QWICKKV 186   | QY 180 QWICKKV 186  |
| Db 181 HGVCCKKV 187   | Db 181 HGVCCKKV 187  | Db 181 HGVCCKKV 187  | Db 181 HGVCCKKV 187  | Db 181 HGVCCKKV 187   |
| RESULT 8  | AAE11759 standard; protein; 189 AA.  | RESULT 9   | ABG05451   | RESULT 9  |
| XX  | AAE11759;  | XX   | ABG05451   | XX  |
| AC  |  | ID   | ABG05451 standard; protein; 843 AA.                                    | ID  |
| XX  | DT   | XX   | ABG05451   | XX  |
| XX  | 18-DEC-2001 (first entry)  | AC   | ABG05451   | AC  |
| DE Human mast cell function associated antigen (MAFA) protein.  | DE Novel human diagnostic protein #5442.   | DE   | DE   | DE  |
| XX  | XX   | XX   | XX   | XX  |
| KW Human; Pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; | KW Human; Pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  |  |  |   |



The invention relates to a novel isolated polypeptide, designated NOVX (NOV1 - 33), consisting of a mature form of one of 61 sequences, given in the specification, or its variant, where amino acid residue(s) in the variant differ from the mature form, provided that the variant differs in not more than 15 % of the amino acids from the sequence of the mature form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and an antibody to the polypeptides, are useful for treating or preventing a NOVX-associated disorder in humans and for treating a syndrome associated with a human disease (NOVX-associated disorder). NOVX polypeptides and the encoding nucleic acids, are useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX polypeptide and polynucleotide, by measuring the level of polypeptide expression or the amount of nucleic acid from a mammal and comparing it with another mammal not having or not predisposed to the disease. NOVX polypeptide is also useful for identifying an agent that binds to NOVX and a cell expressing NOVX is useful for identifying an agent that modulates the expression or activity of NOVX. The antibodies and a polypeptide having 95 % sequence identity to NOVX polypeptide are useful for treating a pathological state in a mammal. The antibodies are also useful for determining the presence or amount of NOVX in a sample. NOVX polypeptides, polynucleotides and antibodies specific for the polypeptides are useful for treating or preventing disorders or syndromes including trauma, viral, bacterial, fungal, protozoal, and parasitic infections. They can also treat disorders such as e.g., Alzheimer's disease or a stroke. The NOVX encoding nucleic acids are useful for expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful for identifying a cell or tissue type in a biological sample, to amplify DNA sequences from very small biological samples such as tissues e.g. hair or skin or body fluids in forensic biology and as primers and probes for use in identifying and/or cloning NOVX homologues in other cell types. The NOVX proteins are useful as an immunogen to generate antibodies which are useful for diagnosing, monitoring protein levels and modulating NOVX activity. Cells comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. The NOVX nucleic acids can be used in gene therapy. This sequence represents a NOVX protein of the invention.

Sequence 191 AA;

Query Match Score 267.5; DB 6; Length 191;  
Best Local Similarity 31.2%; Pred. No. 1.9e-20;  
Matches 59; Conservative 27; N mismatches 80; Indels 23; Gaps 4;

Qy 12 LPEAQVODSRWKLKAVLIRPHS ---RFAMYALGLITVIMSLLMQRILCGGSKDS 67  
Db 12 LPESQFESHQRLVLPIL-EIIVNSKSFRMYSFLGFLTVLVRQLSLAISPRLESGAIA 70

Qy 68 TCSHGPSCPFLWTRNGSHCYFSMERRKKDQWNLKCADKGSIIJTFPDNGYKLFGEYLG 127  
Db 71 HCKKICBPCPTSWLPGGSCYYFSVKTWAEAQGHCADASAHLAAPFDRKVAFYSVLIG 130

Qy 128 QDFYWGLRNLIDGWMEGGPALSRLITLNLQRCGAIH-----NGLOSSCEVA 178  
Db 131 RCLFGIGLARVGGNWWQAPTQI -----DAPAVGGAACFCQUESTSGLPASELRLIE 181

Qy 179 LQWICKKVL 187  
Db 182 KWWHCSKTL 190

RESULT 11  
AAW8267  
ID AAW8267 standard; protein; 99 AA.  
XX  
AC AAW8267;  
XX DT 29-MAR-1999 (first entry)  
XX DE Human MAFa splice variant huMAFa (E3/4-).  
XX

KW Mast cell function-associated antigen; MAFa; huMAFa (E3/4-);  
KW splice variant; human; inflammation; allergy; asthma;  
KW rheumatoid arthritis; tumour; therapy.  
XX  
Homo sapiens.  
OS WO9854209-A2.  
PN XX  
PD 03-DEC-1998.  
XX  
PF 29-MAY-1998;  
XX PR 31-MAY-1997;  
XX PR 97GB-00011148.  
(PEPT-) PEPTIDE THERAPEUTICS LTD.  
PA Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  
PI DR WPI:1999-059806/05.  
XX N-PSDB; AAV8200.  
XX New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  
XX Disclosure; Fig 3; 44pp; English.  
PS This is the amino acid sequence of human mast cell function-associated antigen (MAFa) splice variant huMAFa (E3/4-) which lacks the C-lectin-like domain of human MAFa (see AAW825) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail.  
CC Truncated MAFa polypeptides including huMAFa (E3/4-) and polymuclectides encoding them, as well as synthetic peptides (see AAW825-64, AAW8268-72), can be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and CC asthma), or tumour growth.  
XX Sequence 99 AA;  
SQ Query Match Score 222.5; DB 2; Length 99;  
Best Local Similarity 30.1%; Pred. No. 5.9e-16;  
Matches 56; Conservative 13; N mismatches 28; Indels 89; Gaps 1;

Qy 1 MADSSIYSTLELPAPQVQDESRKIKAVLHRPHISRFAMVALGILTYLMSIJMUYORIL 60  
CC 1 MTDSVITYSMELLPATQAOQNDYGCQQKSSSSRPSSCLVIALGLLTAVILSVLYYQWL 60  
CC 61 CGGSXKDSTSSHCPSCPILWTRNGSHCYFSMERRKKDQWNLKCADKGSIIJTFPDNGYK 120  
CC 61 CQG-----63  
Db 121 LFGEYLGQDFWYIGHRNIDGWRMEGGPALSRLITLNLQRCGAIH-----NGLOSSCEVA 180  
Qy 64 -----ISSNSFVQTGAIITNGLOSSCEVPLH 91  
Db 181 WICKYV 186  
Db 92 WICKYV 97

RESULT 12  
AAW5594  
ID AAW5594 standard; protein; 257 AA.  
XX  
AC AAW5594;  
XX DT 17-OCT-2003 (revised)  
DT 02-MAR-1999 (first entry)  
XX DE Chicken 17.5.3 protein.  
XX KW lectin; carbohydrate; binding; agglutination; selectin; receptor;

KW calcium dependent binding; treatment; cancer; detection; identification;  
 KW CTL-1; ovary; paraganglionic; penis; brain; thyroid; heart.  
 XX  
 OS Gallus gallus.  
 XX  
 PN WO9849306-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US008791.  
 XX  
 PR 29-APR-1997; 97US-00846523.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Bandman O, Shah P;  
 XX  
 DR WPI; 1999-024060/02.  
 DR N-PSDB; AAV83109.  
 XX  
 PT New human C-type lectin and related nucleic acid, vectors, transformed  
 PT cells - antibodies, agonists and antagonists, for diagnosis, prevention  
 PT and treatment of cancers.  
 XX  
 PS Example 3: Page 48-49; 64pp; English.  
 XX  
 CC Chicken 17.5.3 protein shows homology with the human CTL-1 protein.  
 CC Recombinant cells containing expression vectors comprising the CTL-1  
 CC coding sequence can be used to produce recombinant CTL-1 which is useful  
 CC for raising Ab and to screen for specific binding agents. Binding agents  
 CC which are antagonists of CTL-1 can be used to treat or prevent cancer,  
 CC e.g. of ovary, paraganglion, penis, brain, thyroid and heart which are  
 CC associated with overexpression of CTL-1. Fragments of this sequence are  
 CC used to diagnose these conditions, as probes or primers in usual  
 CC hybridisation and/or amplification assays, or for gene mapping, while  
 CC complements of this sequence, antisense or ribozyme sequences are used to  
 CC treat or prevent the aforementioned cancers also. Ab are used directly as  
 CC antagonists or for delivery of therapeutic agents to cells that express  
 CC CTL-1. CTL-1 includes a carbohydrate-recognition domain (aa3-149) and  
 CC also a transmembrane domain, but no secretory signal. CTL-1 also shows  
 CC homology with human CD69 (AAW85593), and mouse CD69 (AAW85595) proteins.  
 CC (Updated on 17-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 257 AA;  
 Query Match 17.7%; Score 182; DB 2; Length 257;  
 Best Local Similarity 28.7%; Pred. No. 5.1e-11;  
 Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;  
 YY 32 RPHLSRPAVALG----LLTVLMSLIMYQRLICGSKDKSTCSPCILWTRNGSHCY 87  
 Db 86 RQRRTVLCAVSAVPMLVIALVAVLQLQFSC--SPRPFFSHV-CPNAWVGQKCY 141  
 Qy 88 YFSMKEKDWNSSLKFCADKGSHLLTDPDNQGVKLFGTYLQDFPYWTGLRNDD---WRWE 144  
 Db 142 YFSDTEDWNSSREHCRIGSLATLDKEEMEFQYQRPADRWGLHRAEGDEHTWVA 201  
 Qy 145 GQPDLSTLRLTSLI-----QRCGAHHRNGQASSEVALQWICKR 185  
 Db 202 DGSA----FTNRPVFELRGGRCAVINGDGISSALCHSEKFVCSR 243  
 XX  
 RESULT 13  
 ID AAW64791 standard; protein; 179 AA.  
 XX  
 AC AAW64791;  
 XX  
 DT 23-NOV-1998 (first entry)  
 XX  
 DE Human Kp43 protein.  
 XX  
 KW Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor;  
 KW cell-mediated cytotoxicity; transplant rejection; autoimmune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5811284-A.  
 XX  
 PD 22-SEP-1998.  
 XX  
 PF 20-MAY-1996; 96US-00650578.  
 XX  
 PR 29-DEC-1993; 93US-00175339.  
 XX  
 PA (SCHERING CORP.  
 PA (LOPEZ-) LOPEZ-BOTET M.  
 PA (BELT-) BELTRAN J A.  
 XX  
 PI Lanier LL, Chang C, Lopez-Botet M, Beltran JA, Phillips JH;  
 XX  
 DR WPI; 1998-530877/45.  
 DR N-PSDB; AAV46476.  
 XX  
 PT DNA encoding natural killer cell surface antigen Kp43 - and transformed  
 PT cells for producing recombinant Kp43.  
 XX  
 PS Claim 1; Col 31-32; 17pp; English.  
 XX  
 CC This sequence represents a novel human natural killer (NK) cell surface  
 CC antigen, Kp43. This sequence can be used in a method resulting in the  
 CC production of recombinant protein expressed by NK and T cells, which may  
 CC inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or  
 CC autoimmune diseases, or may be used to produce antibodies for diagnostic  
 CC or therapeutic use  
 XX  
 SQ Sequence 179 AA;  
 Query Match 17.3%; Score 178.5; DB 2; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 7.5e-11;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;  
 Qy 44 GRITVILMSLIMYQRLICCGS-----KDSCTSHPSCPSPILWTRNGS 84  
 Db 14 GRLGICLISLMMATLGLKNTFTKLSTEPAFTPGPNTELQDSDNC-C-SQEKNVGYRC 70  
 Qy 85 HCYFMSMEKDWNSSLKFCADKGSHLLTDPDNQGVKLFGTYLQDFPYWIGLRNID---GW 141  
 Db 71 NCYFISSEQTKTNESRHLCAQKSSLQQLONTDELDFMSS--SQQPYWIGLSYSEHTAW 128  
 Qy 142 RWEGGPALSRLTN --SLLIQRCGAHHRNG-LQASSCAEVALQWICKVL 187  
 Db 129 LWENGSAQLFSPSFETNTKNCIATYNPNGNALDESCDKNRYICKQQL 178  
 RESULT 14  
 AAW4022  
 ID AAW40222 standard; peptide; 179 AA.  
 XX  
 AC AAW40222;  
 DT 07-JUL-1998 (first entry)  
 XX  
 DE CD94.  
 XX  
 KW TMAH; apoptosis; osteoarthritis; diagnosis; treatment.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9804585-A2.  
 XX  
 PD 05-FEB-1998.  
 XX  
 PR 22-JUL-1997; 97WO-US013077.  
 XX  
 PR 31-JUL-1996; 96US-00690095.

XX (INCY-) INCYTE PHARM INC.  
 PA XX Hillman JL, Au-Young J, Goli SK;  
 XX PI; 1998-130617/12.  
 DR Human macrophage antigen - used for decreasing apoptosis associated with  
 PT osteoarthritis.  
 PT Disclosure; Page 47; 58pp; English.  
 PS XX The type II integral membrane proteins (AAW40219-WA0221) and CD94  
 CC (AAW40222) form a group which has 20% homology with the human macrophage  
 CC antigen (TMAH) (AAW40215). The homology which TMAH shares with this group  
 CC includes a series of disulphide residues. The structural homology between  
 CC the peptides provides information on the structural and physical  
 CC properties of both the TMAH gene and protein. This is used in the  
 CC development of TMAH as a diagnostic tool and as a method of treating  
 CC diseases associated with expression of TMAH  
 XX Sequence 179 AA;  
 SQ Query Match Score 178.5; DB 2; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 7.5e-11; Indels 31; Gaps 7;  
 Matches 54; Conservative 17; Mismatches 68; Sequence 179 AA;  
 XX  
 Qy 44 GLITVILMSILMYORILCGGS----KDSCTCSHCPSCPILWTRNGS 84  
 Db 14 GTLGYICLISIMATGILKNSQKSLKQGKSDC-C-SQCEKRVGVRC 70  
 Qy 85 HCYYFSMEEKDWNSLKFCADKGSHLLTFDNOCVKLFGHGYLGDFYWLGNRID--GW 141  
 Db 71 NCYFISSEQTWNESRHLQSLSLQLQNTDELFMSS--SQOFYWLGSYSEHTAW 128  
 Qy 142 RWEGGPALSRLTN--SLIQRGCAHNG-LQASSCEVALQWICKVU 187  
 Db 129 LWENGSAQLSYLFPSPETFTNPKTAYNPNGNALDESCEDKNRYCKQQL 178  
 RESULT 15  
 ADE76965 ID ADE76965 standard; Protein; 179 AA.  
 XX DT 29-JAN-2004 (first entry)  
 XX DE Human protein expressed in a liver disorder #36.  
 XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;  
 KW tumour; liver; inflammatory disorder; immune response disorder;  
 KW high-throughput screening; differential gene expression; gene therapy.  
 OS Homo sapiens.  
 XX US2003103871-A1.  
 XX PD 12-JUN-2003.  
 XX PF 30-JUL-2001; 2001US-00919039.  
 XX PR 28-JUL-2000; 2000US-0222113P.  
 XX (KASE/) KASER M R.  
 PA Kaser MR;  
 XX PI  
 XX WPI; 2004-031227/03.  
 DR N-PSDB; ADE76964.  
 PT Composition comprising several DNAs that are differentially expressed in  
 PT treated human C3A liver cell cultures, useful for treating liver  
 XX

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OM protein - protein search, using sw model.

Run on: August 10, 2004, 16:18:53 ; Search time 40.2619 Seconds  
(without alignments)  
1464.718 Million cell updates/sec

Title: US-09-811-367B-3  
Scoring table: BLOSUM62  
Perfect score: 1029  
Sequence: 1 MADSSYSTYLELPAPQVQD.....GLQASCEVALQWICKVLY 188

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
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Maximum Match 100%  
Listing first 45 summaries

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 2: /cggn2\_6\_ptodata/2/pubpaas/PCT\_NEW\_PUB.pep:  
 3: /cggn2\_6\_ptodata/2/pubpaas/US06\_PUBCOMB.pep:  
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 Total number of hits satisfying chosen parameters: 1291235

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description         |
|------------|-------|-------|-------|--------|-------------------|---------------------|
| 1          | 1029  | 100.0 | 188   | 9      | US-09-811-367B-3  | Sequence 3, Appli   |
| 2          | 838   | 81.4  | 188   | 9      | US-09-811-367B-5  | Sequence 5, Appli   |
| 3          | 565.5 | 55.2  | 189   | 14     | US-10-125-540-309 | Sequence 196, Appli |
| 4          | 548.5 | 53.3  | 189   | 9      | US-09-811-367B-1  | Sequence 1, Appli   |
| 5          | 182   | 17.7  | 257   | 14     | US-10-125-540-309 | Sequence 4, Appli   |
| 6          | 178.5 | 17.3  | 179   | 10     | US-09-919-019-130 | Sequence 130, Appli |
| 7          | 178.5 | 17.3  | 179   | 15     | US-10-335-009-10  | Sequence 10, Appli  |
| 8          | 173.5 | 16.9  | 199   | 10     | US-09-294-320-86  | Sequence 86, Appli  |
| 9          | 173.5 | 16.9  | 199   | 14     | US-10-207-655-182 | Sequence 182, Appli |
| 10         | 173.5 | 16.9  | 199   | 14     | US-10-179-528-3   | Sequence 3, Appli   |
| 11         | 173.5 | 16.9  | 199   | 15     | US-10-179-127-26  | Sequence 26, Appli  |
| 12         | 171.5 | 16.7  | 231   | 16     | US-10-451-843-1   | Sequence 1, Appli   |
| 13         | 170   | 16.5  | 546   | 12     | US-10-072-012-158 | Sequence 158, Appli |
| 14         | 170   | 16.5  | 549   | 12     | US-10-072-012-160 | Sequence 160, Appli |
| 15         | 168   | 16.3  | 199   | 14     | US-10-179-528-7   | Sequence 7, Appli   |

Sequence 470, App  
Sequence 309, App  
Sequence 25, Appli  
Sequence 2, Appli  
Sequence 23, Appli  
Sequence 300, App  
Sequence 300, App  
Sequence 22, Appli  
Sequence 307, App  
Sequence 307, App  
Sequence 20, App  
Sequence 310, App  
Sequence 22, Appli  
Sequence 98, Appli  
Sequence 98, Appli  
Sequence 88, Appli  
Sequence 88, Appli  
Sequence 14, Appli  
Sequence 4, Appli  
Sequence 90, Appli  
Sequence 305, App  
Sequence 487, App  
Sequence 2, Appli  
Sequence 4, Appli  
Sequence 238, App

ALIGMENTS

RESULT 1  
US-09-811-367B-3  
; Sequence 3, Application US/09811367B  
; GENERAL INFORMATION:  
; Patent No. US2003015510A1  
; APPLICANT: GEMINI SCIENCE, INC.  
; ADDRESS: Takahashi, No. US2003015510Auak1.  
; APPLICANT: Mikayama, Toshiyumi  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MABA)  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MARKING AND USING THE  
; FILE REFERENCE: 011286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811,367B  
; PRIORITY FILING DATE: 2002-03-12  
; PRIORITY NUMBER: 60/190,716  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SEQ ID NO 3  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-09-811-367B-3

Qy 181 WICKKVY 188  
Db 181 WICKKVY 188

RESULT 2  
US-09-811-367B-5  
; Sequence 5, Application US/09811367B  
; Patent No. US20020155110A1  
; GENERAL INFORMATION:  
; APPLICANT: GEMINI SCIENCE, INC.  
; APPLICANT: Takahashi, No.  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MABA)  
; FILE REFERENCE: 021286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811,367B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/190,716  
; PRIORITY FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 188  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; US-09-811-367B-5

Query Match 81.4%; Score 838; DB 9; Length 188;  
Best Local Similarity 80.7%; Pred. No. 1.e-80;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSIYSTLEPAPQVODESRWKLKAVLHRPHLSRFAVALGLTIVLMSLIMYQRII 60  
Db 1 MADNSIYSTLEPAPQVODESRWKLKAVLHRPHLSRFAVALGLTIVLMSLIMYQRII 60

Qy 61 CCGSKDSTCSHCPSPCLWTRNGSHCYFSMEKKDWNSLKFCADKGSHLTIPDNQGVK 120  
Db 61 CCGSKGMCSQSRSRCPCLWTRNGSHCYFSMEKKDWNSLKFCADKGSHLTIPDNQGVK 120

Qy 121 LFGEYLGDFFWIGLNIDGWEEGGPLSLRILTNSLIQRGAIHNGLOSSCEVALQ 180  
Db 121 LFQEYEDFWIGLRIDGWEEGGPLSLRILTNSLIQRGAIHNGLOSSCEVALQ 180

Qy 181 WICKKVU 187  
Db 181 WICEKVU 187

RESULT 3  
US-10-207-655-196  
; Sequence 196, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Hayden-Ledbetter, Martha S.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390067-401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 196  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-207-655-196

Query Match 55.2%; Score 568.5; DB 14; Length 189;  
Best Local Similarity 57.2%; Pred. No. 5.7e-52;  
Matches 107; Conservative 25; Mismatches 54; Indels 1; Gaps 1;

RESULT 4  
US-09-811-367B-1  
; Sequence 1, Application US/09811367B  
; Patent No. US20020155110A1  
; GENERAL INFORMATION:  
; APPLICANT: GENINI SCIENCE, INC.  
; APPLICANT: Takahashi, No. US20020155110A1uaki  
; APPLICANT: Miyakawa, Toshihumi  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MABA)  
; FILE REFERENCE: 021286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811,367B  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 60/190,716  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-811-367B-1

Query Match 54.3%; Score 548.5; DB 9; Length 189;  
Best Local Similarity 55.6%; Pred. No. 7.5e-50;  
Matches 104; Conservative 26; Mismatches 56; Indels 1; Gaps 1;

Qy 1 MADSSIYSTLEPAPQVODESRWKLKAVLHRPHLSRFAVALGLTIVLMSLIMYQRII 60  
Db 1 MADNSIYSTLEPAPQVODESRWKLKAVLHRPHLSRFAVALGLTIVLMSLIMYQRII 60

Qy 61 CCGSKDSTCSHCPSPCLWTRNGSHCYFSMEKKDWNSLKFCADKGSHLTIPDNQGVK 120  
Db 61 CCGSKGMCSQSRSRCPCLWTRNGSHCYFSMEKKDWNSLKFCADKGSHLTIPDNQGVK 120

Qy 121 LFGEYLGDFFWIGLNIDGWEEGGPLSLRILTNSLIQRGAIHNGLOSSCEVALQ 180  
Db 121 LLQVSEAFWIGRNNSGWREDGSPLNSFVQTCAINNGLOSSCEVPL 180

Qy 180 QWICKKV 186  
Db 181 HGVKKKV 187

RESULT 5  
US-10-179-528-4  
; Sequence 4, Application US/1017-528  
; Publication No. US20030166136A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive

CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 943 04  
 COMPUTER READEABLE FORM:  
 COMPUTER: IBM Compatible  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq For Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/179, 528  
 FILING DATE: 24-Jun-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/846, 523  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billing, Lucy J  
 REGISTRATION NUMBER: 36,749  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-845-0555  
 TELEX: 415-845-4166  
 TELEFAX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 257 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 505325  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 S-10-179-528-4

Query Match 17.7%; Score 182; DB 14; Length 257;  
 Best Local Similarity 28.7%; Pred. No. 8.3e-11;  
 Matches 48; Conservative 25; Mismatches 72; Indels 22; Gaps 6;

Y 32 RPHLSRFAMYALG----LLTILMORYIRLCCGSKDSTCSCPILWTRNGSHCY 87  
 Y 86 RQNRRLVCAVALAVCMVLVALVTPRSPSC -SPRPFFSHY -CPNAWVGFOQKCY 141

Y 88 YFSMEKKDNNSSLKPCADKGSHLTFPDNQGVKLGEYLGODFYWIGLRNIDG---WRVE 144  
 Y 142 YFSDTDSWNSREHCHRGSLATLTKEEMEFM1QYQRADRNLHRAEGDBHWTWA 201

Y 145 GGPALSRLITNLSI-----QRCGAHRNGLOASSCEVALQWICKK 185  
 Y 202 DGSA---FTNRPVFELRGGRCAVINGISSSAUCHSERFWCSR 243

RESULT 6  
 US-09-919-039-130  
 Sequence 130, Application US/09919039  
 Publication No. US20030108871A1  
 GENERAL INFORMATION:  
 APPLICANT: Kaser, Matthew R  
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
 FILE REFERENCE: PA-0035 US  
 CURRENT APPLICATION NUMBER: US/09/919, 039  
 CURRENT FILING DATE: 2002-09-09  
 PRIOR APPLICATION NUMBER: 60/222, 113  
 PRIOR FILING DATE: 2000-07-28  
 NUMBER OF SEQ ID NOS: 401  
 SOFTWARE: PERL Program  
 SEQ ID NO: 130  
 LENGTH: 179  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: misc feature  
 NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CDU  
 US-09-919-039-130

Query Match 17.3%; Score 178.5; DB 10; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 1.3e-10;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7

Y 44 GLITVILMSLMLYQRLICCGS-----KDSTSHPSCPILWTRNGS 84  
 Y 14 GLTGICLCSLMATLGILKNSFTKLSIEPAFTPGPNTELQKSDC-C-SCQEVKGYRC 70

Y 85 HCYYFSMEKKDNNSSLKPCADKGSHLTFPDNQGVKLGEYLGODFYWIGLRNID--GW 141  
 Y 71 NCYFISSEQKTWNESRHLQASQSKSLQLQNTDEDFMS --SOQFYWIGLSYSEEHHTAW 128

Y 142 RWEGGPALSRLITN--SLIQRCAHNRG-LQASSCEVALQWICKKVL 187  
 Y 129 LWNGSALSQYLFPSFETENTKNCAINPQNGNALDESCDKRICKQQL 178

RESULT 7  
 US-10-315-009-10  
 ; Sequence 10, Application US/10335009  
 ; Publication No. US2004001804A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Portmelloor , Mathew A.  
 ; APPLICANT: Boles, Kent S.  
 ; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION  
 ; FILE REFERENCE: 11207/02/46987-7  
 ; CURRENT APPLICATION NUMBER: US/10/335, 009  
 ; CURRENT FILING DATE: 2002-12-31  
 ; PRIOR APPLICATION NUMBER: US 09/475, 365  
 ; PRIOR FILING DATE: 1999-12-30  
 ; NUMBER OF SEQ ID NO: 11  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 10  
 ; LENGTH: 179  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-335-009-10

Query Match 17.3%; Score 178.5; DB 15; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 1.3e-10;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7

Y 44 GLITVILMSLMLYQRLICCGS-----KDSTSHPSCPILWTRNGS 84  
 Y 14 GLTGICLCSLMATLGILKNSFTKLSIEPAFTPGPNTELQKSDC-C-SCQEVKGYRC 70

Y 85 HCYYFSMEKKDNNSSLKPCADKGSHLTFPDNQGVKLGEYLGODFYWIGLRNID--GW 141  
 Y 71 NCYFISSEQKTWNESRHLQASQSKSLQLQNTDEDFMS --SOQFYWIGLSYSEEHHTAW 128

Y 142 RWEGGPALSRLITN--SLIQRCAHNRG-LQASSCEVALQWICKKVL 187  
 Y 129 LWNGSALSQYLFPSFETENTKNCAINPQNGNALDESCDKRICKQQL 178

RESULT 8  
 US-09-284-320-86  
 ; Sequence 86, Application US/09284320  
 ; Publication No. US20030092175A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kato, Seishi et al.  
 ; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs  
 ; FILE REFERENCE: GIN-6705CPUS  
 ; CURRENT APPLICATION NUMBER: US/09/284, 320  
 ; CURRENT FILING DATE: 1999-06-21  
 ; PRIOR APPLICATION NUMBER: JP B-301429  
 ; PRIOR FILING DATE: 1998-11-13  
 ; PRIOR APPLICATION NUMBER: PCT/JP97/04056  
 ; PRIOR FILING DATE: 1997-11-07

NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-284-320-86

Query Match 16.9%; Score 173.5; DB 10; Length 199;  
Best Local Similarity 23.8%; Pred. No. 4.8e-10;  
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

Qy 3 DSSISTYLEPAPOVQDESRWKLAVALHRPHLSR-  
Db 11 NSSIH----PESGQENDAT----SPHFSTRHEGSFQVBPVLCAVMNNVFTILII 51  
Qy 52 SL-LMYQRLICGSKDSTC--SHCPSCPILWTRNGSHCYFSMEKWDNSSLIKFCADK 106  
Db 57 ALIALSVAQYQNCPGQTFSMPSDSHVSQCCSEDWGYQRKCYFISTVRSWTSQAQSEH 116  
Qy 107 GSHLTFPDNQTVKLFRGEYLQDFWIGRNIDS--WRWEGGPALSRLI-LTNSLIQRCG 163  
Db 117 GATLAVIDSEKDMMFLKRYAGREEMWGLKEPGRPWKSNGKEFNNWFNTGGS--DKCV 174

Qy 164 AIIHRNGLQASSEVALQWICK 185  
Db 175 FLRNTEVSSMCECKNLWICNK 196

RESULT 9  
US-10-207-655-182  
; Sequence 182, Application US/10207655  
; Publication No US2003018592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; INVENTION: Binding DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 393069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; CURRENT FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 182  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-182

Query Match 16.9%; Score 173.5; DB 14; Length 199;  
Best Local Similarity 23.8%; Pred. No. 4.8e-10;  
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

Qy 3 DSSISTYLEPAPOVQDESRWKLAVALHRPHLSR-  
Db 11 NSSIH----PESGQENDAT----SPHFSTRHEGSFQVBPVLCAVMNNVFTILII 51  
Qy 52 SL-LMYQRLICGSKDSTC--SHCPSCPILWTRNGSHCYFSMEKWDNSSLIKFCADK 106  
Db 57 ALIALSVAQYQNCPGQTFSMPSDSHVSQCCSEDWGYQRKCYFISTVRSWTSQAQSEH 116  
Qy 107 GSHLTFPDNQTVKLFRGEYLQDFWIGRNIDS--WRWEGGPALSRLI-LTNSLIQRCG 163  
Db 117 GATLAVIDSEKDMMFLKRYAGREEMWGLKEPGRPWKSNGKEFNNWFNTGGS--DKCV 174

Qy 164 AIIHRNGLQASSEVALQWICK 185  
Db 175 FLRNTEVSSMCECKNLWICNK 196

RESULT 10  
US-10-179-528-3  
; Sequence 3, Application US/10179528  
; Publication No. US20030166136A1

RESULT 11  
US-10-379-127-26  
; Sequence 26, Application US/10379127  
; General Information:  
; APPLICANT: Emtage, Peter C.R.  
; APPLICANT: Drmanac, Radivoje  
; APPLICANT: Goodrich, Rylee

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Shah, Purvi  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/179, 528  
FILING DATE: 24-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/846, 523  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36, 749  
REFERENCE/DOCKET NUMBER: PE-0281 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-445-4166  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 199 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 29188  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-179-528-3

Query Match 16.9%; Score 173.5; DB 14; Length 199;  
Best Local Similarity 23.8%; Pred. No. 4.e-10;  
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

Qy 3 DSSISTYLEPAPOVQDESRWKLAVALHRPHLSR-  
Db 11 NSSIH----PESGQENDAT----SPHFSTRHEGSFQVBPVLCAVMNNVFTILII 51  
Qy 52 SL-LMYQRLICGSKDSTC--SHCPSCPILWTRNGSHCYFSMEKWDNSSLIKFCADK 106  
Db 57 ALIALSVAQYQNCPGQTFSMPSDSHVSQCCSEDWGYQRKCYFISTVRSWTSQAQSEH 116  
Qy 107 GSHLTFPDNQTVKLFRGEYLQDFWIGRNIDS--WRWEGGPALSRLI-LTNSLIQRCG 163  
Db 117 GATLAVIDSEKDMMFLKRYAGREEMWGLKEPGRPWKSNGKEFNNWFNTGGS--DKCV 174

Qy 164 AIIHRNGLQASSEVALQWICK 185  
Db 175 FLRNTEVSSMCECKNLWICNK 196

|                                  |                               |  |
|----------------------------------|-------------------------------|--|
| Qy                               | 176 EVALQWICK 184             | Sequence 158, Application US/10072012      |
|                                  |                               | Publication No. US20040033493A1            |
|                                  |                               | GENERAL INFORMATION:                       |
| ; APPLICANT: Tchernev, Velizar Y |                               |  |
|                                  |                               | ; APPLICANT: Spytter, Kimberly             |
|                                  |                               | ; APPLICANT: Zerhusen, Bryan               |
|                                  |                               | ; APPLICANT: Fatturajan, Meera             |
|                                  |                               | ; APPLICANT: Shimkets, Richard             |
|                                  |                               | ; APPLICANT: Li, Li                        |
|                                  |                               | ; APPLICANT: Gangoli, Esha                 |
|                                  |                               | ; APPLICANT: Padigaru, Muralidhara         |
|                                  |                               | ; APPLICANT: Anderson, David W.            |
|                                  |                               | ; APPLICANT: Rastelli, Luca                |
|                                  |                               | ; APPLICANT: Miller, Charles E.            |
|                                  |                               | ; APPLICANT: Gerlich, Valerie              |
|                                  |                               | ; APPLICANT: Taupier Jr, Raymond J.        |
|                                  |                               | ; APPLICANT: Gusev, Vladimir Y.            |
|                                  |                               | ; APPLICANT: Colman, Steven D.             |
|                                  |                               | ; APPLICANT: Wolenc, Adam R.               |
|                                  |                               | ; APPLICANT: Pena, Carol E. A              |
|                                  |                               | ; APPLICANT: Furtak, Katarzyna             |
|                                  |                               | ; APPLICANT: Grossie, William M.           |
|                                  |                               | ; APPLICANT: Alsobrook II, John P.         |
|                                  |                               | ; APPLICANT: Lepley, Denise M.             |
|                                  |                               | ; APPLICANT: Rieger, Daniel K.             |
|                                  |                               | ; APPLICANT: Burgess, Catherine E.         |
|                                  |                               | ; TITLE OF INVENTION: Proteins and Nuc     |
|                                  |                               | ; FILE REFERENCE: 21402-258                |
|                                  |                               | ; CURRENT APPLICATION NUMBER: US/10/072012 |
|                                  |                               | ; CURRENT FILING DATE: 2002-01-31          |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/265,102     |
|                                  |                               | ; PRIOR FILING DATE: 2001-01-30            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/265,514     |
|                                  |                               | ; PRIOR FILING DATE: 2001-01-31            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/265,517     |
|                                  |                               | ; PRIOR FILING DATE: 2001-01-31            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/265,412     |
|                                  |                               | ; PRIOR FILING DATE: 2001-01-31            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/265,395     |
|                                  |                               | ; PRIOR FILING DATE: 2001-01-31            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/266,406     |
|                                  |                               | ; PRIOR FILING DATE: 2001-02-02            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/266,767     |
|                                  |                               | ; PRIOR FILING DATE: 2001-02-05            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/267,057     |
|                                  |                               | ; PRIOR FILING DATE: 2001-02-07            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/266,975     |
|                                  |                               | ; PRIOR FILING DATE: 2001-02-07            |
|                                  |                               | ; PRIOR APPLICATION NUMBER: 60/267,459     |
|                                  |                               | ; REMAINING PRIOR APPLICATION DATA REMOVED |
|                                  |                               | ; NUMBER OF SEQ ID NOS: 1391               |
|                                  |                               | ; SOFTWARE: PatentIn Ver. 2.1              |
|                                  |                               | ; SEQ ID NO: 158                           |
|                                  |                               | ; LENGTH: 546                              |
|                                  |                               | ; TYPE: PRT                                |
|                                  |                               | ; ORGANISM: Homo sapiens                   |
| Qy                               | 79 WTRNGSHCYFYSMEKDNSSLKF     | Score 16.5%                                |
| Qy                               | 79 WKENGGSLLYVSSVKSWSHEAEFOC  | Score 16.5%                                |
| Db                               | 417 WKENGGSLLYVSSVKSWSHEAEFOC | Score 16.5%                                |

QY 137 NIDG-WRWEPPALSRLITNSLQRGA-----IHRNG----LOAS---SC 175  
 Db 477 GTEGSWRTDGTTP-----NAAQNKGFWENQSDDNWRKNGTEDCVQIQQXWNNDTC 529

QY 176 EVALQWICKK 185  
 Db 530 DTPXQWCKK 539

RESULT 14  
 US-10-072-012-160  
 ; Sequence 160, Application US/10072012  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Tchernev, Velizar  
 ; APPLICANT: Spytak, Kimberly  
 ; APPLICANT: Zerhusen, Bryan  
 ; APPLICANT: Paturyan, Meera  
 ; APPLICANT: Shimkets, Richard  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Gangoli, Baha  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Miller, Charles E.  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Taupier Jr, Raymond J.  
 ; APPLICANT: Gusev, Vladimir Y.  
 ; APPLICANT: Colman, Steven D.  
 ; APPLICANT: Wolencz, Adam R.  
 ; APPLICANT: Pena, Carol B. A  
 ; APPLICANT: Furtak, Katarzyna  
 ; APPLICANT: Grossé, William M.  
 ; APPLICANT: Alsobrook II, John P.  
 ; APPLICANT: Lepley, Denise M.  
 ; APPLICANT: Rieger, Daniel K.  
 ; APPLICANT: Burgess, Catherine E.  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 2A402-258  
 ; CURRENT APPLICATION NUMBER: US/10/072,012  
 ; CURRENT FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: 60/265,102  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: 60/265,514  
 ; PRIOR FILING DATE: 2001-01-31  
 ; PRIOR APPLICATION NUMBER: 60/265,517  
 ; PRIOR FILING DATE: 2001-01-31  
 ; PRIOR APPLICATION NUMBER: 60/265,412  
 ; PRIOR FILING DATE: 2001-01-31  
 ; PRIOR APPLICATION NUMBER: 60/265,395  
 ; PRIOR FILING DATE: 2001-02-07  
 ; PRIOR APPLICATION NUMBER: 60/266,406  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 60/266,767  
 ; PRIOR FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: 60/267,057  
 ; PRIOR FILING DATE: 2001-02-07  
 ; PRIOR APPLICATION NUMBER: 60/266,975  
 ; PRIOR FILING DATE: 2001-02-07  
 ; PRIOR FILING DATE: 2001-02-08  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NO: 1391  
 ; SOFTWARE: PatentInVer. 2.1  
 ; SEQ ID NO: 160  
 ; LENGTH: 549  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-072-012-160

QY Matches 39; Conservative 17; Mismatches 44; Indels 30; Gaps 6;  
 QY 79 WTRNGSHCYFSEMEKDNSSSLKFCDGSHLLTFPDNQGVLFGEYLGQDFPWIGL--R 136  
 Db 420 WKGGSLYYSVSYKKSPTHEAEQFCVSQGAHLASVASKEQALVEFTSKVYIWGLTDR 479  
 QY 137 NIDG-WRWEPPALSRLITNSLQRGA-----IHRNG----LOAS---SC 175  
 Db 480 GTBGSWRRTDGTFP-----NAAQNKGFWENQSDDNWRKNGTEDCVQIQQXWNNDTC 529

QY 176 EVALQWICKK 185  
 Db 533 DTPXQWCKK 542

RESULT 15  
 US-10-179-528-7  
 ; Sequence 7, Application US/10179528  
 ; Publication No. US2003016136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Shan, Furui  
 ; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Portor Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/179,528  
 ; FILING DATE: 24-Jun-2002  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0281 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; TELEX: <Unknown>  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 199 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 584907  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-10-179-528-7

Query Match 16.3%; Score 168; DB 14; Length 199;  
 Best Local Similarity 24.1%; Pred. No. 1.9e-09;  
 Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 5;

QY 38 FAMVAIGLTLTVLMSL-----MYQRLLCGSKDSTCSCPILWTRNGSHC 86  
 Db 43 WAVLIVVLTSLLITALIAJVGKKNCPGLYEKL-----ESSDHVATCKNEWISYKRTC 96  
 QY 87 YYFSMEKDNSSSLKFCDGSHLLTFPDNQGVLFGEYLGQDFPWIGL-----IDGWRWE 144

Db 97 YFFSTTTKSWALLAQRSCEADAATLAVTDSKDMTFLKRYSGELEHWIGLKNEANQTMKWA 156  
Qy 145 GGPAL-SLRLLTNSLIQRGATIHRNGLASSCPEVALONTCKR 185  
Db 157 NGKEFNSWPNLTGS--GRCVSYNHKNVTAVDCEANFHWCSC 196

Search completed: August 10, 2004, 16:32:37  
Job time : 41.2619 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.6407 Seconds  
 (without alignments)  
 662.924 Million cell updates/sec

Title: US-09-811-367B-3

Perfect score: 1029

Sequence: 1 MADSSIYSTLELPAPQVQD.....GLQASSCEVALQWICKKVLY 188

Scoring table: BLOSUM62

Gapext 0.5

Scored:

Searched: 389414 seqs, 5162571 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA\_\*

1: /cgm2\_6/ptodata/2/iaia/5A\_COMB.pep:  
 2: /cgm2\_6/ptodata/2/iaia/5B\_COMB.pep:  
 3: /cgm2\_6/ptodata/2/iaia/6A\_COMB.pep:  
 4: /cgm2\_6/ptodata/2/iaia/6B\_COMB.pep:  
 5: /cgm2\_6/ptodata/2/iaia/PECTUS\_COMB.pep:  
 6: /cgm2\_6/ptodata/2/iaia/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description        |
|------------|-------|-------|-------|--------|-------------------|--------------------|
| 1          | 838   | 81.4  | 188   | 3      | US-09-722-126A-5  | Sequence 5, Appli  |
| 2          | 838   | 81.4  | 188   | 5      | PCT-US95-04558-5  | Sequence 5, Appli  |
| 3          | 551   | 53.5  | 114   | 3      | US-08-722-126A-6  | Sequence 6, Appli  |
| 4          | 551   | 53.5  | 114   | 5      | PCT-US95-04258-6  | Sequence 6, Appli  |
| 5          | 267   | 25.9  | 76    | 4      | US-09-531-056A-23 | Sequence 23, Appli |
| 6          | 178.5 | 17.3  | 179   | 1      | US-08-60-035-9    | Sequence 9, Appli  |
| 7          | 178.5 | 17.3  | 179   | 2      | US-08-650-578-2   | Sequence 2, Appli  |
| 8          | 178.5 | 17.3  | 179   | 2      | US-08-688-742-3   | Sequence 3, Appli  |
| 9          | 178.5 | 17.3  | 179   | 2      | US-09-113-788-3   | Sequence 3, Appli  |
| 10         | 178.5 | 17.3  | 179   | 3      | US-08-789-9       | Sequence 9, Appli  |
| 11         | 173.5 | 16.9  | 199   | 5      | PCT-US93-10418-2  | Sequence 2, Appli  |
| 12         | 168   | 16.3  | 199   | 5      | PCT-US93-10418-4  | Sequence 4, Appli  |
| 13         | 164   | 16.0  | 225   | 2      | US-08-738-432-2   | Sequence 2, Appli  |
| 14         | 164.5 | 16.0  | 225   | 5      | PCT-US94-07587-2  | Sequence 2, Appli  |
| 15         | 163.5 | 15.9  | 191   | 4      | US-09-531-056A-6  | Sequence 6, Appli  |
| 16         | 160.5 | 15.6  | 231   | 1      | US-08-690-095-6   | Sequence 6, Appli  |
| 17         | 160.5 | 15.6  | 231   | 3      | US-09-113-789-6   | Sequence 6, Appli  |
| 18         | 160.5 | 15.6  | 231   | 3      | US-08-543-246B-6  | Sequence 6, Appli  |
| 19         | 160.5 | 15.6  | 231   | 3      | US-08-543-246B-23 | Sequence 2, Appli  |
| 20         | 154   | 15.0  | 190   | 4      | US-09-127-946-14  | Sequence 14, Appli |
| 21         | 153   | 14.9  | 316   | 3      | US-09-111-470-4   | Sequence 4, Appli  |
| 22         | 152   | 14.8  | 1479  | 3      | US-08-622-052-2   | Sequence 2, Appli  |
| 23         | 152   | 14.8  | 122   | 3      | US-08-722-126A-9  | Sequence 9, Appli  |
| 24         | 152   | 14.8  | 122   | 5      | PCT-US95-04558-9  | Sequence 9, Appli  |
| 25         | 152   | 14.8  | 215   | 1      | US-08-590-095-7   | Sequence 7, Appli  |
| 26         | 152   | 14.8  | 215   | 3      | US-09-113-789-7   | Sequence 7, Appli  |
| 27         | 152   | 14.8  | 215   | 3      | US-08-543-246B-16 | Sequence 16, Appli |

## ALIGNMENTS

RESULT 1  
 US-09-722-126A-5  
 ; Sequence 5, Application US/08722126A  
 ; Patent No. 6034227  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PECHT, Israel  
 ; APPLICANT: GUTHMANN, Marcelo D.  
 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MARA)  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 ; STREET: 419 Seventh Street N.W., Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/722-126A  
 ; FILING DATE: 08-OCT-1996  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04258  
 ; FILING DATE: 06-APR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 109257  
 ; FILING DATE: 08-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: PECHT-1A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 628-5197  
 ; FAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 188 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-722-126A-5  
 ; Query Match Score 838; DB 3;  
 ; Best Local Similarity 80.7%; Pred. No. 1.8e-86;

Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0; Qy 1 MADSSISTLELPAPQODESRWKAVLHRPHLSFAMVALGLIVLMSILMYCIRL 60 Db 1 MADNSIYSTLELPAPQODDSRKVAVLHRPCVSTLVMAVLGLIVLMSILYQRTL 60 Qy 61 CGCSKDKSTSHCPSCPCLLWTRGSHCYFSMEEKDWNSSLKFCADKGSHLLTFPDNGGVK 120 Db 61 CGSGKGFMCSQCSRCPNLMRNGSHCYFSMERRDNSSLKFCADKGSHLLTFPDNGVN 120

RESULT 3 US-08-722-126A-6

Qy 121 LPGEYLQDGFYWLGNRIDGWREGGPALSRLTNTSLIQRGGAHNRGLQASSCEVALQ 180 Db 121 LPGEYVGDFYWLGNRIDGWREGGPALSRLTNTSLIQRGGAHNRGLQASSCEVALQ 180

Qy 121 LPGEYLQDGFYWLGNRIDGWREGGPALSRLTNTSLIQRGGAHNRGLQASSCEVALQ 180 Db 121 LPGEYVGDFYWLGRDGDWRMEDGPAISLTSNSVVQCGTIIHRCGLHASSCEVALQ 180

Qy 181 WICKKV 187 Db 181 WICEKV 187

RESULT 2 PCT-US95-04258-5

i Sequence 5, Application PC/TU9504258

/ GENERAL INFORMATION:

/ APPLICANT:

/ TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

/ TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL

/ NUMBER OF SEQUENCES: 10

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: BROWDY AND NEIMARK

/ STREET: 419 Seventh Street, N.W., Suite 300

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: USA

/ ZIP: 20004

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US95/04258

/ FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: IL 109257

/ FILING DATE: 08-APR-1994

/ ATTORNEY/AGENT INFORMATION:

/ NAME: BROWDY, Roger L.

/ REGISTRATION NUMBER: 25, 618

/ REFERENCE/DOCKET NUMBER: PECHT=1A

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (202) 628-5197

/ TELEFAX: 202-737-3528

/ INFORMATION FOR SEQ ID NO: 5:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 188 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

PCT-US95-04258-5

Query Match 81.4%; Score 838; DB 5; Length 188;

Best Local Similarity 80.7%; Pred. No. 1..8e-86;

Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MADSSISTLELPAPQODESRWKAVLHRPHLSFAMVALGLIVLMSILMYCIRL 60 Db 1 MADNSIYSTLELPAPQODDSRKVAVLHRPCVSTLVMAVLGLIVLMSILYQRTL 60

Qy 61 CGCSKDKSTSHCPSCPCLLWTRGSHCYFSMEEKDWNSSLKFCADKGSHLLTFPDNGGVK 120 Db 61 CGSGKGFMCSQCSRCPNLMRNGSHCYFSMERRDNSSLKFCADKGSHLLTFPDNGVN 120

RESULT 4 PCT-US95-04258-6

Sequence 6, Application PC/TUSS504255  
 GENERAL INFORMATION:  
 APPLICANT: TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
 NUMBER OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BRODY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1., Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04258  
 FILING DATE: 06-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 109257  
 FILING DATE: 08-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BRODY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: PECHT=1 PCT  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 TELEX: 248633  
 SEQUENCE FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 114 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT/US95/04258-6

Query Match 53.5%; Score 551; DB 5; Length 114;  
 Best Local Similarity 84.1%; Pred. No. 2e-5+;  
 Matches 95; Conservative 9; Indels 0; Gaps 0;

Qy 75 CPIIWTNGHCHYYSMEKDWNSLKFADKGSHLLTPDNGYKLFGPYLGDFWY 134  
 Db 1 CPNLWMRNGHCHYYSMEKDWNSLKFADKGSHLLTPDNGYNLFQEVYGGDFWY 60

Qy 135 LRNTDGWRMEGPALSRLILTNSLIQRCAIHNRGLQASSCEVALQWICKV 187  
 Db 61 LRDIDGWRNEDGPALSLSILSNSVVQKCGTHRCGLHASSCEVALQWICKV 113

RESULT 5  
 US-09-531-056A-23  
 Sequence 23, Application US/09531056A  
 Patent No. 6455683  
 GENERAL INFORMATION:  
 APPLICANT: Bristol-Myers Squibb Company  
 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI  
 TITLE OF INVENTION: PROTEINS  
 FILE REFERENCE: DB200 NP  
 CURRENT APPLICATION NUMBER: US/09/531,056A  
 CURRENT FILING DATE: 2000-03-20  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 23  
 LENGTH: 76  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-531-056A-23

Query Match 25.9%; Score 267; DB 4; Length 76;  
 Best Local Similarity 59.5%; Pred. No. 1.2e-22;  
 Matches 44; Conservative 10; Indels 0; Gaps 0;

Qy 73 PSCPPLWTRNGSHCYFSMEKDWNSLKFADKGSHLLTPDNGYKLFGPYLGDFWY 132  
 Db 1 PSCPPLWTRNGSHCYFSMEKDWNSLKFADKGSHLLTPDNGYKLFGPYLGDFWY 60

Qy 133 IGLRNIDGPRWEGG 146  
 Db 61 IGLRNMSGPRWEDG 74

RESULT 6  
 US-09-690-095-9  
 Sequence 9, Application US/08690095  
 Patent No. 5792648  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Golli, Surya K.  
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/690,095  
 FILING DATE: Filed Herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0110 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-855-4166  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 119 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 IMMEDIATE SOURCE: GenBank  
 LIBRARY: GenBank  
 CLONE: 1098617

Query Match 17.3%; Score 178.5; DB 1; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 3.5e-12;  
 Matches 54; Conservative 17; Indels 31; Gaps 7;

Qy 44 GLUTYLMILLMTCRILCGGS-----KDISTCSHCPSCPILWTRNGS 84  
 Db 14 GTLGICLISLMATIGLILKNSPKLSSIAFTGPNNIQLQKDSDC--SCQBRKWGYRC 70

Qy 85 HCXYFSMEKDWNSLKFADKGSHLLTPDNGYKLFGPYLGDFWY 141  
 Db 71 NCYTSSEQTKWNESEHLCASOKSSLLQQTNDLDEMSS--SQFWYGLSYSEHTDWA 128

Qy 142 RWEQQPALSRLITN--SLIQRGGAIRNG-LQASSCEVALWICKV 187  
 Db 129 LWENGSAQLFFSFETPNKNCLAYNNGNALDESCDNRYICKQOL 178

RESULT 7  
US-08-650-578-2  
Sequence 2, Application US/08650578  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Chiwen  
; APPLICANT: Aramburu Beltran, Jose  
; APPLICANT: Lopez-Botet, Miguel  
; APPLICANT: Phillips Jr., Joseph H.  
; APPLICANT: Lanier, Lewis L.  
TITLE OF INVENTION: Purified Mammalian NK Antigens and Related Reagents  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentRelease #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,578  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,339  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
PRIORITY DATA:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match 17.3%; Score 178.5; DB 2; Length 179;  
Best Local Similarity 31.8%; Pred. No. 3.5e-12;  
Matches 54; Conservative 17; Mismatches 66; Indels 31; Gaps 7;

RESULT 8  
US-08-688-342-3  
Sequence 3, Application US/08688342  
; GENERAL INFORMATION:  
; Patent No. 5871964  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:

APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/688,342  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0095-1 CTP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1098616  
US-08-688-342-3

Query Match 17.3%; Score 178.5; DB 2; Length 179;  
Best Local Similarity 31.8%; Pred. No. 3.5e-12;  
Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLITVIMSLIMYQLILCGS-----KDISTCSHCPSCPILWTRNGS 84  
Db 14 GRIGIICLISLMATGLILKNSPTKLISIEPAFTPGPNELQKDSDC-C-SCOEKWVGYRC 70  
Qy 85 HCYYSMEKKDWSSLKFCADGSHLTFPDNOGVKLFGEYLGQDFWIGRNID--GW 141  
Db 71 NCFISSEQKTTWNEHLCASQKSSLQLQNTDELDMSS--SQQFWIGLSSYSEHTAW 128

RESULT 9  
US-09-113-788-3  
Sequence 3, Application US/09113788  
; GENERAL INFORMATION:  
; Patent No. 5963104  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,788  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/688,342  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0110 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: Peptide  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617  
 US-09-113-789-9

Query Match 17.3%; Score 179.5; DB 3; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 3.5e-12;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLITVILMSLIMYQRLCCGS----KDSTOSHCPSCPILWTRNGS 84  
 Db 14 GTLGICLISMLATIGKNSFTKUSIEPARTPGPNIELQKDSO-C-SQEQKVGYRC 70

Query Match 17.3%; Score 178.5; DB 2; Length 179;  
 Best Local Similarity 31.8%; Pred. No. 3.5e-12;  
 Matches 54; Conservative 17; Mismatches 68; Indels 31; Gaps 7;

Qy 44 GLITVILMSLIMYQRLCCGS----KDSTOSHCPSCPILWTRNGS 84  
 Db 14 GTLGICLISMLATIGKNSFTKUSIEPARTPGPNIELQKDSO-C-SQEQKVGYRC 70

RESULT 11  
 PCT-US93-10418-2  
 Sequence 2, Application PC/TUS9310418  
 GENERAL INFORMATION:  
 APPLICANT: Ziegler, Steven F.  
 APPLICANT: Hjerrild, Kathryn A.  
 TITLE OF INVENTION: Activation Antigen CD69  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/10418  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2610-WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-09-113-789-9  
 Sequence 9, Application US/09113789  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Goli, Surya K.  
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,789  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/690,095

i MOLECULE TYPE: protein  
PCT-US93-10418-2

Query Match 16.9%; Score 173.5; DB 5; Length 199;  
Best Local Similarity 23.8%; Pred. No. 1..5e-11;  
Matches 48; Conservative 36; Mismatches 83; Indels 35; Gaps 8;

Qy 3 DSSYSTLELPAPQVQDESRWKLKAVLHRPHLSR-----FAMVALGLLTILM 51  
Db 11 NSSIH-----PESQENDAT-----SPHFSTRETFEGSFQPVLAIVNNVFTILLI 56  
Qy 52 SL--LMYORILKCCGSKDSTC---SHCPSCPILTRNGSHCYYSMEKCDWNSSLKFCAKD 106  
Db 57 ALIALSVQOYNCPGQTFSMPSDHVSQSCSDWVGYQRKCYFSTVRSWTSAQNACSEH 116  
Qy 107 GSHTLTFDNOGYKLFGYLGQDFYIGURNLDG--NEWEGGPALSRLI-LTNSLIRCG 163  
Db 117 GATLAVIDSEKONNFKRYAGREHWWGLKEPGHPWKWSNGKEFNWFENVTCG--DKCV 174  
Qy 164 AHRNGLQASSCEVALQICKK 185  
Db 175 FLRNTEVSSMECKNLWICNK 196

---

RESULT 12  
PCT-US93-10418-4  
; Sequence 4, Application PC/TUUS9310418  
; GENERAL INFORMATION:  
; APPLICANT: Ziegler, Steven F.  
; APPLICANT: Hjerrild, Kathryn A.  
; TITLE OF INVENTION: Activation Antigen CD69  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738,462  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,435  
REFERENCE/DOCKET NUMBER: DX0397  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08/738-162-2

Query Match 16.0%; Score 164.5; DB 2; Length 225;  
Best Local Similarity 27.4%; Pred. No. 1.8e-10;  
Matches 60; Conservative 32; Mismatches 90; Indels 37; Gaps 10;

Qy 1 MADDSITVSTLEIP--EAPQ-----VQDESRWLKLVAVLHRPHLSREAMVALGI--- 45  
Db 1 MDQQAIVAYELNPITDSDPESSSSPSSPLRDVCQGPWHQFAL---KLSAGJILLVVVT 56

Qy 46 -LTWILMSLMMQRILCCG---SKDSTCSH--CPSCPILTRNGSHCYFSMERKDWN 97  
Db 57 GLSVSVTSLLIKSISIEKCSVVDIQSQSNKTTBPGLNCPVQLREKCLFLSHTVNPNW 116

Query Match 16.0%; Score 168; DB 5; Length 199;  
Best Local Similarity 24.1%; Pred. No. 6.2e-11;  
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 5;

Qy 38 FAMVALGLLTILM-----MYQRLCCGSKDSTCSHCPSCPILTRNGSHC 86  
Db 43 WAVLIVLUTSIIALLNVSKYNCYKLI-----ESDDHMYATCANEWISTKRT 96

Qy 87 YFSMEEKCDWNSSLKFCADKGSHLITFPDNQGYKLFGEYBLQDFYNGLRLN--IDGWRME 144  
Db 176 NDLEIRSDAKENSCISIQTSTSYSEVCSTEWRICQKEL 214

RESULT 14  
 PCT-US94-07587-2  
 Sequence 2, Application PC/TUS94/07587  
 GENERAL INFORMATION:  
 APPLICANT: Schering Corp.  
 TITLE OF INVENTION: PURIFIED MAMMALIAN NK ANTIGENS AND RELATED REAGENTS  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Schering Corp.  
 STREET: One Giralda Farms  
 CITY: Madison  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07240  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.1  
 SOFTWARE: Microsoft Word 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US94/07587  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lunn, Paul G.  
 REGISTRATION NUMBER: 32,743  
 REFERENCE/DOCKET NUMBER: DX0397K  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7255  
 TELEFAX: 201-822-7039  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 225 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US94-07587-2

Query Match 15.9%; Score 163.5%; DB 4; Length 191;  
 Best Local Similarity 25.3%; Pred. No. 1.9e-10;  
 Matches 50; Conservative 21; Mismatches 78; Indels 49; Gaps 7;

QY 11 ELPAPQVQDESRWKLVKAVLHRPHLSRFAVMVALGLTVI-LMSLMYQRTILCGG-----63  
 Db 15 ELPAPGCHHSKEHSIKA-----TULWRLFLIMELTIVGMAAL 56

QY 64 -SKSQTCSHOPS----CPILWIRNGSHCYTSMEKKDWNSLKFCDKGSHLITFDNN 116  
 Db 57 SALTRANCHQEPSPVCLQAAPESWIGFQRKCFYFSDDTKWTSSQRFCDSQDADIAQVESF 116

QY 117 QGVKLFGETYLGQDGYWIGRNIDS-MWWEWG-----PALSRLILTNSLIQRGAIIHR 167  
 Db 117 QELNELLRYKGPSDHWIGSREQQPWKRWINGTEWTRQFPLG-----AGECAYLND 168

QY 168 NGLOSSCEVALQWICKK 185  
 Db 169 KGASSARHYTERKWCISK 186

Search completed: August 10, 2004, 16:20:31  
 Job time : 14.6407 secs

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RESULT 15  
 US-09-531-056A-6  
 Sequence 6, Application US/09531056A  
 GENERAL INFORMATION:  
 APPLICANT: Bristol-Myers Squibb Company  
 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLX PROTEINS AND THEIR SOLUBLE FUSI FILE REFERENCE: DB20 NP  
 CURRENT APPLICATION NUMBER: US/09/531,056A  
 CURRENT FILING DATE: 2000-03-20  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.0

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## OM protein - protein search, using sw model

Run on: August 10, 2004, 16:12:27 ; Search time 11.9788 Seconds  
 (without alignments) 1509.673 Million cell updates/sec

Title: US-09-811-367B-5  
 Perfect score: 1036  
 Sequence: 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78:\*

1: Pirr:\*

2: Pirr:\*

3: Pirr:\*

4: Pirr:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description  |
|------------|-------|-------------|--------|----------|--|
| 1          | 1036  | 100.0       | 188    | 2 I59421 | mast cell function<br>lymphocyte early a<br>gene 17.5 protein<br>natural killer cell<br>NKR-P1 protein -<br>NKR-P1 protein hom<br>hepatocyte lectin 2 -<br>natural killer cell<br>NKR-P1 protein hom<br>NK-cell receptor P<br>asialoglycoprotein<br>C type lectin, B 1<br>phospholipase-A(2)<br>natural killer cell<br>asialoglycoprotein<br>lectin galactose/<br>HRV gp120-binding<br>scavenger receptor<br>lectin M-ASGP-BP<br>type II lectin-like<br>agkisacutacin beta<br>natural killer cell<br>B-cell surface ant<br>secretory phosphol<br>secretory phosphol<br>asialoglycoprotein<br>natural killer cell<br>hepatocyte lectin - r<br>hepatocyte lectin hom |
| 2          | 184.5 | 17.8        | 199    | 2 JH0822 | lymphocyte early activation antigen AIM/CD69 - human<br>Species: Homo sapiens (man)  |
| 3          | 184   | 17.8        | 257    | 2 A46467 | C;Date: 30-Aug-1994 #sequence revision 20-Aug-1994 #text_change 08-0ct-1999<br>C;Accession: JH0822; IS6073; R;Lopez-Cabrer, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M   |
| 4          | 172.5 | 16.7        | 227    | 2 I38700 | J. Exp. Med. 178, 537-547, 1993<br>A;Title: A secretory inhibitory signal transduction molecule on mast cells is another C<br>A;Reference number: 159421; MUID:9601676; PMID:568140<br>A;Status: preliminary;<br>A;Molecule type: mRNA<br>A;Cross-references: EMBL:X79812; NID:91020141; PIDN:CAA56208.1; PID:91020142<br>C;Genetics:<br>A;Gene: mafa  |
| 5          | 169.5 | 16.4        | 225    | 2 I46467 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 6          | 167   | 16.1        | 223    | 2 I46467 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 7          | 165.5 | 16.0        | 301    | 2 I46467 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 8          | 162.5 | 15.7        | 170    | 2 T28140 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 9          | 159.5 | 15.4        | 220    | 2 C46467 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 10         | 159   | 15.4        | 223    | 2 A35917 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 11         | 159.5 | 15.4        | 301    | 2 S13165 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 12         | 158   | 15.3        | 156    | 2 T28141 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 13         | 158   | 15.3        | 1487   | 2 S48719 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 14         | 157   | 15.2        | 216    | 2 PT0375 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 15         | 156   | 15.1        | 284    | 2 S29855 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 16         | 154.5 | 14.9        | 304    | 2 JX0209 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 17         | 153.5 | 14.8        | 404    | 2 A46274 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 18         | 153   | 14.8        | 742    | 2 JC7595 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 19         | 148.5 | 14.3        | 306    | 2 A42230 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 20         | 148   | 14.3        | 237    | 2 JC7608 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 21         | 146   | 14.1        | 146    | 2 JG7135 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 22         | 142.5 | 13.8        | 233    | 2 PT0372 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 23         | 142.5 | 13.8        | 359    | 2 A43532 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 24         | 141.5 | 13.7        | 1326   | 2 B56395 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 25         | 141.5 | 13.7        | 1465   | 2 A56395 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 26         | 140.5 | 13.6        | 311    | 1 LNUH2A | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 27         | 139   | 13.4        | 240    | 2 I54524 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 28         | 139   | 13.4        | 284    | 1 LNRTL  | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |
| 29         | 137   | 13.2        | 167    | 1 WNVZF2 | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188<br>Best Local Similarity 100.0%; Pred. No. 3.2e-90;<br>Matches 188; Conservative 0; Mismatches 0;<br>Indels 0; Gaps 0;   |

## ALIGNMENTS

| RESULT 1 |   |   |   |   |   |
|----------|---|---|---|---|---|
| 159421   | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188               |
|          | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0;          | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0;          | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0;          | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0;          | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0;          |
| Qy       | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188               |
| Db       | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188               |
| Qy       | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188               |
| Db       | 61 CGCGSKGFMCQSQCSCPNLWMRNGSHYFSMEKRDWNSSLKFCADKGSHULTFPDPNQGVN 120 |
| Qy       | 121 LFQEYVGDFWIGRDIQGRWEDGPALSLSLTSVYOKCGTPVTHRCGLHASSEVALQ 180     |
| Db       | 121 LFQEYVGDFWIGRDIQGRWEDGPALSLSLTSVYOKCGTPVTHRCGLHASSEVALQ 180     |
| Qy       | 181 WICEKVLP 188  |
| Db       | 181 WICEKVLP 188  |

| RESULT 2  |  |  |  |  |  |
|---|--|--|--|--|--|
| JH0822  | 1 MADNSIYSTLELPAAFPVQD.....GLHASSCEVALQWICKEVKLVP 188      |
|   | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0; | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0; | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0; | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0; | Best Local Similarity 100.0%;保守性匹配 0;不匹配 0;插入 0;删除 0;缺口 0; |
| C;Species: Homo sapiens (man)   |  |  |  |  |  |
| C;Accession: JH0822; IS6073; R;Lopez-Cabrer, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M |  |  |  |  |  |
| A;Title: Molecular cloning, expression, and chromosomal localization of the human early<br>mitting receptors.       |  |  |  |  |  |
| A;Reference number: 159422; MUID:9334030; PMID:83440758   |  |  |  |  |  |
| A;Accession: JH0822;  |  |  |  |  |  |
| A;Molecule type: mRNA   |  |  |  |  |  |

A;Residues: 1-199 <LOP>  
A;Cross-references: GB:G397938; PIDN:CAA80298.1; PID:9397939  
A;Note: the authors translated the codon CAA for residue 110 as Glu  
R.Hamann, J.; Fiebig, H.; Strauss, M.  
J. Immunol. 150, 4920-4927, 1993  
A;Title: Expression cloning of the early activation antigen CD69, a type II integral mem  
A;Reference number: 156167;  
A;Accession: 156167  
A;Status: translated from GB/EMBL/DDBj  
A;Molecule type: mRNA  
A;Cross-references: GB:L07555; PIDN:AB46359.1; PID:9291898  
R.Santis, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.  
Eur. J. Immunol. 24, 1692-1697, 1994  
A;Title: Structure of the gene coding for the human early lymphocyte activation antigen  
 receptors.  
A;Residue: 1-199 <RES>  
A;Accession: 660753  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residue: 1-199 <SAN>  
A;Cross-references: ENBL:230426; PIDN:CAA80217.1; PID:9553352  
C;Comment: This protein is the earliest inducible cell surface glycoprotein expressed in  
C;Genetics:  
A;Gene: GDB:CD69  
A;Cross-references: GDB:132925; OMIM:107273  
A;Map references: 12P13-12P12  
C;Superfamily: C-type lectin homology  
C;Keywords: Glycoprotein; phosphoprotein; receptor; transmembrane protein  
F:39-64;Domain: transmembrane #status predicted <TM>  
F:85-194;Domain: C-type lectin homology <LCH>  
F:18/30;Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status Predicted  
F:1/1;Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status Predicted  
F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match Score 17.8%; Best Local Similarity 26.3%; Pred. No. 4.7e-10;  
Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;  
Query Match Score 184.5%; Best Local Similarity 26.3%; Pred. No. 4.7e-10;  
Matches 35; Conservative 30; Mismatches 76; Indels 9; Gaps 4;  
Query Match Score 184.5%; Best Local Similarity 26.3%; Pred. No. 4.7e-10;  
Matches 45; Conservative 30; Mismatches 76; Indels 9; Gaps 4;  
Query Match Score 185%; Best Local Similarity 28.6%; Pred. No. 6.8e-10;  
Matches 162; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

RESULT 4  
A46467  
natural killer cell receptor P1 - mouse  
N;Alternate name: NKR-P1 protein  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Jun-1993 #sequence revision 19-Feb-1999 #text\_change 05-May-2000  
C;Accession: A46467; A46456  
R.Giorda, R.; Trucco, M.  
J. Immunol. 147, 1701-1708, 1991  
A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill  
A;Reference number: A46467; MUID:91349596; PMID:1880421  
A;Accession: A46467  
A;Molecule type: mRNA  
A;Residues: 'MHLLCT'1-227<G10>  
A;Cross-references: GB:MM77676; PID:9200058  
A;Experimental source: A-JAK protein  
A;Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBIP:52379); the sequence  
R.Giorda, R.; Weisberg, E.P.; Ip, T.K.; Trucco, M.  
J. Immunol. 149, 1957-1963, 1992  
A;Title: Genomic structure and strain-specific expression of the natural killer cell re  
A;Reference number: A46502; MUID:92388663; PMID:1517565  
A;Accession: A46502  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-109, 'H'111-181, 'D'183-227 <G12>  
A;Cross-references: GB:X64716; PID:9533395; PIDN:CAA45971.1; PID:9817989  
A;Experimental source: BALB/c 3T3 fibroblastoid cell line  
A;Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIP:113072  
R.Yokoyama, W.M.; Ryan, J.C.; Hunter, J.J.; Smith, H.R.; Stark, M.; Seaman, W.E.  
J. Immunol. 147, 3229-3235, 1991  
A;Title: cDNA cloning of mouse NKR-P1 and genetic linkage with Ly-49. Identification of  
A;Reference number: A46456; MUID:92013158; PMID:1680927  
A;Accession: A46456  
A;Molecule type: mRNA  
A;Residues: 1-38, 'L'40-227 <YOK>  
A;Cross-references: GB:M7753; PIDN:AAA39366.1; PID:9198570  
A;Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBIP:60431)  
C;Superfamily: natural killer cell receptor P1; C-type lectin homology <LCH>  
P,94-210/Domain: C-type lectin homology <LCH>

Query Match Score 16.7%; Best Local Similarity 24.4%; Pred. No. 7.2e-09;  
Matches 53; Conservative 35; Mismatches 86; Indels 43; Gaps 8;

Qy 6 TYSTLEPAAPRQVDDSSRKWV-----KAVHLRCPVSYLMVALGLLTIVMLSLI 54  
Db 6 VYFGLXPRPTPGAWHEPPSLPPDACRCPRSRSHRSALKLSCAGLILV---VTLIGMSVL 61  
Qy 55 -----LYQRTLQCGSKGFMCSQRCPNLWWRNGSHCYFSMERDWNSS 99  
Db 62 VRVLIQKPSIEKCYLQENL--NKTIDCSAKLEPQDWLSHRKCFHYSQVSNTWEQG 118  
Qy 100 LKPCADKGSHLITFPDNQGVNLFEQYVGEDF-YWIGLR---DIDGWRWEDGPALS--- 150  
Db 119 LVDGDKGATMLIQDQEELRFIDSIEKEKTNFWIGLRTLPDM-WKWNIGSTLNNSDV 177

RESULT 3  
I50146  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: 150146  
R.Berniot, A.; Zoorob, R.; Auffray, C.  
Immunogenetics 39, 221-229, 1994  
A;Title: Linkage of a new member of the chicken lectin supergene family to the chicken Mhc genes  
A;Reference number: 150146; MUID:9416469.; PMID:8119728  
A;Accession: I50146  
A;Status: preliminary; translated from GB/EMBL/DDBj  
A;Molecule type: mRNA  
A;Residues: 1-257 <BR>  
A;Cross-references: GB:MM8072; PIDN:9505324; PIDN:AAA48558.1; PID:9505325  
C;Superfamily: C-type lectin homology  
F:129-241/Domain: C-type lectin homology <LCH>

Query Match Score 17.8%; Best Local Similarity 28.6%; Pred. No. 6.8e-10;  
Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

Qy 151 LSILSNSSVVKCGGTHRCGLHASCEVALQWCEKV 187  
Db 178 LKTTGDTENDSCAAISGDKVTFESCNDSRNWCKEEL 214

|   |   |   |   |
|---|---|---|---|
| RESULT 5  |   | QY 102 FCADKGSHLILTEFDNQGVNLQFQYYVGEDE--YWIGLRL---DIDGWRWEDGPALS---LS 152<br>I38700 hNKR-P1a protein - human<br>C;Species: Homo sapiens (man)<br>C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999<br>C;Accession: I38700<br>R;Immunol. 153, 2417-2428, 1994.<br>A;Title: Human NKR-P1A: A disulfide-linked homodimer of the C-type lectin superfamily expressed in natural killer cell receptor p1; C-type lectin homology<br>F;94-210/Domain: C-type lectin homology <Lch>  | Db 121 DCGRGATILLIPQQEERFLDSIKREKNSFWGLRTLPDNW-WKWNITTFNSDVLK 179 |
| RESULT 6  |   | QY 153 ILSNSVQKCGTIIHRCLHASSEVALQVICRYL 187<br>Db 180 ITGTENGSCASISGDKVTSCESTDNRWICQKEL 214   |   |
| RESULT 7  | LNRT2   | Query Match 16.4%; Score 169.5; DB 2; Length 225;<br>Best Local Similarity 26.1%; Pred. No. 1.4e-08;<br>Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;<br>A;Residues: 1-225 <RES><br>A;Cross-references: EMBL:U11276; NID:9538220; PID:AAA21605.1; PMID:9544496<br>C;SuperFamily: natural killer cell receptor p1; C-type lectin homology<br>F;94-210/Domain: C-type lectin homology <Lch>   |   |
| Query Match 16.4%; Score 169.5; DB 2; Length 225;<br>Best Local Similarity 26.1%; Pred. No. 1.4e-08;<br>Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;<br>A;Residues: 1-225 <RES><br>A;Cross-references: EMBL:U11276; NID:9538220; PID:AAA21605.1; PMID:9544496<br>C;SuperFamily: natural killer cell receptor p1; C-type lectin homology<br>F;94-210/Domain: C-type lectin homology <Lch> | QY 1 MADNSIYSTELP-----AAPRVQDDSRPWKVAVHLRPC--VSYLYMVALGIL 46<br>Db 1 MDQQAIVAFENLNPPTDSGPSSSPSSPSSPPTDQGSPFWH-QFAALKSCAGIILVLYVVTG-L 58       | A;Accession: B28462<br>A;Molecule type: protein<br>A;Residues: 1-301 <HAL><br>A;Cross-references: GB:J02762; NID:g205162; PID:g205163<br>A;Molecule type: mRNA<br>A;Accession: B28462<br>A;Molecule type: protein<br>A;Residues: 88-96, 'X', '88-118, 'X', '120-129-158-177-182, 'X', '184, 'X', '186-189-192-290, 'C', 29<br>R;Sanford, J.P.; Elliott, R.W.; Doyle, D.<br>DNA 7, 721-728, 1988<br>A;Title: Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.<br>A;Reference number: A31601; PMID:89170119; PMID:3234178<br>A;Accession: A31601<br>A;Molecule type: mRNA<br>A;Residues: 1-301 <SAN><br>A;Cross-references: GB:X07636; NID:g57066; PIDN:CAA30476.1; PMID:g57067<br>R;McPhail, M.; Berg, P.<br>Mol. Cell. Biol. 7, 1841-1847, 1987<br>A;Title: Identification and characterization of cDNA clones encoding two homologous pro<br>A;Reference number: A26888; PMID:87257885; PMID:3.600647<br>A;Accession: A26888<br>A;Molecule type: protein<br>A;Residues: 1-152, 'A', '154-201, 'I', '203-259, 'C', '261-301 <MDP><br>A;Cross-references: GB:MI634; NID:g206648; PIDN:CAA203B.1; PMID:g206649<br>C;SuperFamily: the authors translated the codon GCA for residue 153 as Arg and ATT for residue R;Drickamer, K.; Marion, J.P.; Bierns, G.; Leung, J.O.<br>J. Biol. Chem. 259, 770-778, 1984<br>A;Title: Primary structure of the rat liver asialoglycoprotein receptor: structural evi<br>A;Reference number: A25417; PMID:84111554; PMID:6319386<br>A;Accession: A25417<br>A;Molecule type: protein<br>A;Residues: 201-259, 'C', 261-281 'ND'<br>C;Comment: Calcium is required for ligand binding.<br>C;SuperFamily: hepatic lectin; C-type lectin homology<br>C;Keywords: endocytosis, glycoprotein; lectin; liver; receptor; transmembrane protein<br>F;61-77/Domain: intracellular #status predicted <INT><br>F;78-301/Domain: extracellular #status predicted <TRN><br>F;170-293/Domain: C-type lectin homology <Lch><br>F;97,119,165/Binding site: carbohydrate (Asn) (covalent) #status predicted<br>Query Match 16.0%; Score 165.5; DB 1; Length 301;<br>Best Local Similarity 27.3%; Pred. No. 4.4e-08;<br>Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3; |   |
| Query Match 16.1%; Score 167; DB 2; Length 223;<br>Best Local Similarity 23.3%; Pred. No. 2.3e-08;<br>Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;  | QY 58 RTLCGCGSKGFMCSQCSRCPNLMWRNGSHCYYSMFKRDWNSSLKCADGSHLITFPDNO 117<br>Db 153 RTLTCAOFFLUSNGTBCCPWNVEFGSCTWFSRDLTWAEDQVQCMENAHLLVINSRE 212   |   |   |
| Query Match 16.1%; Score 167; DB 2; Length 223;<br>Best Local Similarity 23.3%; Pred. No. 2.3e-08;<br>Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;  | QY 118 GVNLQFQYYVGEDEFYWGLRIDG-WRWEDEGPALSSTLSNSVVQ-----KCG 133<br>Db 213 EQEFVTKHRAFHTWGLTDKGSWVQWDTEYRNFKWNAFTQDPDNWGHEEGGSEDC 272          |   |   |
| Query Match 16.1%; Score 167; DB 2; Length 223;<br>Best Local Similarity 23.3%; Pred. No. 2.3e-08;<br>Matches 50; Conservative 34; Mismatches 91; Indels 40; Gaps 8;  | QY 47 TVILMSLILYORTLCCG----SKGFMCSQCSRCPNLMWRNGSHCYYSMFKRDWNSSLK 101<br>Db 61 VLVLSVQKSSVQKICADVQENRTHTDCSVNLECPDQWLSHRDCKCFRVEQVSNTWEQGA 120 |   |   |

Qy 164 TIHRCGGL-HASSCEVALQWICER 185  
 Db 273 EILSDGWLNDFCQVNWACER 295

**RESULT 8**  
 T28140 natural killer cell receptor homolog - chicken (fragment)  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 R;Name, S.; Kaufman, J.; Beck, S.  
 submitted to the EMBL Data Library, May 1998  
 A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex  
 A;Accession number: Z20475  
 A;Cross-references: EMBL:AL023516; NID:e1292539; PIDN:CAA18960.1  
 A;Experimental source: clone cB12  
 C;Genetics:  
 A;Map position: 16  
 A;Note: Intron positions not resolved (incomplete sequence)

Query Match Score 15.4%; DB 2; Length 220;  
 Best Local Similarity 25.3%; Pred. No. 1.2e-07;  
 Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

Qy 27 KAVLHRPCVSYLIVVALGLLTIVMLIYL-----QRTLCCGSKGMCSQCSR-----74  
 Db 38 RLALKLSPAGLILIV----LIGMSVLIVRLVYQKPSSEBKCC---VFTQENLNRKTIVNLE 90

Qy 75 CPNLMRNGSHCYXFMSMEKRDWNNSSLKFCAKGSHLITFPDNGQVNLQEYVGDFE-YW 132  
 Db 91 CPODWLHRDKCPTHVSQSYNTWEQADCGRKCATLILIQDQELRFLLDSIKEKYNFW 150

Qy 133 IGR-----DIDGTRWEDGPALSISLNSNSVVK---GCTIHRCGLHASCEVALQWICER 185  
 Db 151 IGRFETLPDMN-WKWLNGTTENSVDLKUTPESCASTLGDKUTPESCASTLGVITENGSCAS 209

Qy 186 VL 187  
 Db 210 EL 211

**RESULT 10**  
 A35917 NK-cell receptor P1 - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 24-Sep-1999  
 C;Accession: A35917  
 R;Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M.  
 Science 249, 1298-1300, 1990  
 A;Title: NKR-P1, a signal transduction molecule on natural killer cells.  
 A;Reference number: A35917; PMID:90378305; PMID:2399464  
 A;Accession: A35917  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-223 <GTO>  
 A;Cross-references: GB:MG62891; NID:9205722; PIDN:AAA41710.1; PMID:9205723  
 C;Superfamily: natural killer cell receptor P1; C-type lectin homology  
 F;94-210/Domain: C-type lectin homology <LCH>

Query Match Score 15.4%; DB 2; Length 223;  
 Best Local Similarity 23.5%; Pred. No. 1.2e-07;  
 Matches 39; Conservative 33; Mismatches 73; Indels 21; Gaps 5;

Qy 38 LYVALGLLTIVMS-----LILYQRTLCCGSKGMCSQCSRNLWNRNGSHCYVF 89  
 Db 54 LAIVGMSILVRVYQKPSVEPRVLIQENLSKTPGPAKL----KCPKDWLSHRDCKFHV 108

Qy 90 SMEKRDWNNSSLKFCAKGSHLITFPDNGQVNLQEYVG--EDFYWGHLR---DIDGWRWE 144  
 Db 109 SQTSITWKESSAADCGGRKATLILQDQEEBLRFLNLTKRISSTFWGSLSYTLSDENWKWI 168

Qy 145 DGPALS--LSLISNSVYQKGTLTHRCGLHASCEVALQWICERVL 187  
 Db 169 NGSTLNSDVLSSITGDTKDSASVSDKVLSESCDSDNIWVQKEL 214

**RESULT 9**  
 C46467 NK-P1 protein homolog gene-40 - mouse  
 N;Alternative names: natural killer cell activation molecule; NK1.1 alloantigen  
 C;Species: Mus musculus (house mouse)  
 C;Accession: C46467; #sequence\_revision 18-Jun-1993 #text\_change 24-Sep-1999  
 R;Giorda, R.; Trucco, M.  
 J. Immunol. 147, 1701-1708, 1991  
 A;Title: A family of genes selectively coexpressed in adherent lymphokine-activated kill  
 A;Reference number: A46467; MUID:91349596; PMID:1880421  
 A;Accession: A46467  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-220 <GLO>  
 A;Cross-references: GB:MT77678; NID:9200062; PIDN:AAA39824.1; PMID:9200063  
 A;Experimental source: NK cells, C57BL/2J  
 A;Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBI:P:52383)  
 R;Ryan, J.C.; Turck, J.; Niemi, E.C.; Yokoyama, W.M.; Seaman, W.E.  
 J. Immunol. 149, 1631-1635, 1992  
 A;Title: Molecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of natur  
 A;Reference number: A46499; MUID:92373004; PMID:1506685  
 A;Accession: A46499  
 A;Status: Preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-86, 90-220 <RYA>  
 A;Cross-references: GB:SA3141; NID:9254094; PIDN:AB22979.1; PMID:9254095  
 A;Experimental source: C57BL/6J NK cells  
 A;Note: sequence extracted from NCBI backbone (NCBIN:111622, NCBI:P:111624)  
 C;Superfamily: natural killer cell receptor P1; C-type lectin homology

**RESULT 11**  
 S13165 asialoglycoprotein receptor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Accession: S13165  
 R;Sanford, J.P.; Doyle, D.  
 Biochim. Biophys. Acta 1087, 259-261, 1990  
 A;Title: Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor gene  
 A;Accession: S13165  
 A;Reference number: S13165; MUID:91027942; PMID:2223888  
 A;Accession: S13165  
 A;Molecule type: mRNA

A;Residues: 1-301 <SAN>  
A;Cross-references: EMBL:X53042; NID:953104; PIDN:CAA37211.1; PID:953105  
C;Species: hepatic lectin; C-type lectin homology  
C;Keywords: Glycoprotein; liver; transmembrane protein  
F;170-293/Domain: C-type lectin homology <LCH>

Query Match 15.4%; Score 159.5; DB 2; Length 301;  
Best Local Similarity 26.6%; Pred. No. 1.6e-07; Indels 15; Gaps 3;  
Matches 38; Conservative 23; Mismatches 67; Gaps 5;

QY 58 RTLCGGSKGFMCSQCSRCPNLWNRNGSHCYFSMEKRDNSSLKFCADKGSHLLTFPDNQ 117  
Db 153 RTLTCQLATEFQSNBCCPQVNPWBEGGSCTWFSIDGLTAEDOYCQLENHLLIVNSRE 212  
QY 118 GVNLQEQYQEDFWMGRDIDG-WRWEQDPAISLISLNSVUQ 163  
Db 213 EQDFVVKHRSQFHLMGRDIDG-LDRDGSKWKWIDTDXRSNYRNWAFTQPDNWQGHEDQGGEODA 272  
QY 164 TIRHRCG-LHASCEVALQWICKEK 185  
Db 273 EILSDQHAWDNPCQVNWRVCEK 295

RESULT 14  
p0375 natural killer cell receptor group 2-D - human

N;Alternate names: integral membrane protein NK2-D  
C;Species: Homo sapiens (man)  
C;Accession: PT0375; S115671; S1110  
R;Houchins, J.P.; Yabe, T.; McSharry, C.; Bach, F.H.  
J. Exp. Med. 173, 1017-1020, 1991  
A;Title: DNA sequence analysis of NK2-D, a family of related cDNA clones encoding type I  
A;Reference number: P10372; MUID:91178434; PMID:2007850  
A;Accession: PT0375  
A;Molecule type: mRNA  
A;Residues: 1-216 <HOU>  
A;Cross-references: EMBL:X54870; NID:935062; PIDN:CAA38652.1; PID:935063  
A;Experimental source: natural killer cell  
A;Note: translation of nucleotide sequence is not complete  
C;Keywords: transmembrane protein

Query Match 15.2%; Score 157; DB 2; Length 216;  
Best Local Similarity 26.4%; Pred. No. 2e-07; Indels 62; Gaps 6;  
Matches 42; Conservative 33; Mismatches 62; Gaps 6;

QY 35 VSYLVMVALGLLTVYLMLSLXORTLCGSKGFMCSQCSRCPNLWMRNGSHCYFSMEKR 94  
Db 65 IRFIMVA-IWSAFLNSLFNQVQIPLR---SYCPCPKWNWICYKNNCQFDDEK 118  
QY 95 DWNSSLKECADKGSHLLTFPDNQGVNLFEQYVGDFYNIQLRDI- -DGWRWEDGPALSL 151  
Db 119 NWYESQASCMNSQNASSLLKVYSKEDQDLRK-LVRSYHNGLVLHPTNGSWQEDGILSP 176

Query Match 15.3%; Score 158; DB 2; Length 156;  
Best Local Similarity 27.5%; Pred. No. 1.2e-07; Indels 10; Gaps 4;  
Matches 33; Conservative 22; Mismatches 55; Gaps 4;

QY 72 CSRCPNLWNRNGSHCYFSMEKRDNSSLKFCADKGSHLLTFPDNQGVNLFEQYVGDEY 131  
Db 27 CAQQPFDFWIGFRGCKYKQPFSEDESWTSSONNCASIAVAFDSAELISFTMHKGSSPH 86

QY 132 WIGRIDLIG --- WRWEQDPAISLISLNSVQVKCGTHRCGLHASSCEVALQWICKEK 185  
Db 87 WVGL-SREGKEHPWNVNPSLHLFQVQGDGL---CAVLDAGLSSSSCSTRNWCTK 142

RESULT 15  
S29355 asialoglycoprotein receptor 1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Accession: S29355  
R;Takezawa, R.; Shinzawa, K.; Watanabe, Y.; Akaike, T.  
Biochim. Biophys. Acta 1172, 220-222, 1993  
A;Title: Determination of mouse major asialoglycoprotein receptor cDNA sequence.  
A;Reference number: S23855; MUID:93176818; PMID:8439366  
A;Accession: S29355  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-284 <TAK>  
A;Cross-references: EMBL:D13517; NID:9220480; PIDN:BAA02734.1; PID:9220481  
C;Superfamily: hepatic lectin; C-type lectin  
C;Keywords: glycoprotein; transmembrane protein

RESULT 13  
S48719 phospholipase-A(2) receptor protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Accession: S48719  
R;Higashino, K.; Ishizaki, J.; Kishino, J.; Ohara, O.; Arita, H.  
Eur. J. Biochem. 225, 375-382, 1994  
A;Title: Structural comparison of phospholipase-A(2)-binding regions in phospholipase-A  
A;Reference number: S48719; MUID:95010128; PMID:7925459  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-148 <HIG>  
A;Cross-references: GB:D10779; NID:91375042; PIDN:9691754  
C;Superfamily: phospholipase A2 receptor; C-type lectin homology  
C;Keywords: phospholipase A2 receptor; C-type lectin; C-type lectin; transmembrane protein

P;153-276/Domain: C-type lectin homology &lt;LCH&gt;

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Query Match      15.1%; Score 156; DB 2; Length 284;
Best Local Similarity 25.6%; Pred. No. 3. 2e-07;
Matches 41; Conservative 20; Mismatches 75; Indels 24; Gaps 4;

Qy   52 SLLYQRTLCCGSKGFMG-----SQCSRCPNLMRNGSHCYFSMERDWNSSILKF 102
     ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   121 SLLHVVQLVSDYRSLSQMAAFRGNSERTCOPINVEYEGSCYNNSSSRPWTEDKY 180
     : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   103 CADRGSHILTEPDNQGYNLFQEYVGEDFYWIGLRDIDG-WRNEDGPALSLSLS----- 155
     : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   181 CQLENALIUVVVTSRDQNFLQRHMGPNTWIGLTDQNGPWWKWDGTIDYETGFQNWRPEQP 240
     : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy   156 -NSVVKCGTIIHRCGIHAASS-----CEVALQWICKVL 187
     : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   241 DNWYGHGLGGGEDCAHHFTIDGRWNDDVCRRPYRWCTKL 280
     : | : | : | : | : | : | : | : | : | : | : | : | : |

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Search completed: August 10, 2004, 16:19:36  
 Job time : 11.9788 secs

| Scoring table:   | BLOSUM62                       | Gapop 10.0 , Gapext 0.5 |                      |
|--|--------------------------------|-------------------------|----------------------|
| Searched:  | 141681 seqs, 52070155 residues |                         | 141681               |
| Total number of hits satisfying chosen parameters:   |                                |                         |                      |
| Minimum DB seq length: 0   |                                |                         |                      |
| Maximum DB seq length: 2000000000  |                                |                         |                      |
| Post-processing: Maximum Match 0%  |                                |                         |                      |
| Post-processing: Minimum Match 100%  |                                |                         |                      |
| Database :   | SwissProt_42::*                |                         |                      |
| Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |                                |                         |                      |
|  |                                |                         | SUMMARIES            |
| Result No.   | Score                          | Query                   | Description          |
|  |                                | Match Length            | DB ID                |
| -  | -                              | -                       | -                    |
| 1  | 184.5                          | 17.8                    | CD69_HUMAN           |
| 2  | 172.5                          | 16.7                    | CD69_MOUSE           |
| 3  | 167.1                          | 16.1                    | NK11_MOUSE           |
| 4  | 163.5                          | 15.8                    | NK12_MOUSE           |
| 5  | 161.5                          | 15.6                    | CD94_MACMU           |
| 6  | 159.5                          | 15.4                    | LECI_RAT             |
| 7  | 159.5                          | 15.4                    | NK14_MOUSE           |
| 8  | 159.5                          | 15.4                    | NKL3_RAT             |
| 9  | 159.5                          | 15.3                    | LECI_MOUSE           |
| 10   | 157.1                          | 15.2                    | CD69_MACMU           |
| 11   | 155.0                          | 15.0                    | CD94_HUMAN           |
| 12   | 155.0                          | 17.9                    | CD94_PANTR           |
| 13   | 154.9                          | 14.9                    | MNGL_MOUSE           |
| 14   | 154.9                          | 14.9                    | V239_FOWPV           |
| 15   | 154.9                          | 14.9                    | CD69_MOUSE           |
| 16   | 154.9                          | 14.9                    | LBCH_MOUSE           |
| 17   | 153.5                          | 14.8                    | CLE2_HUMAN           |
| 18   | 152.0                          | 14.7                    | NKGE_PANTR           |
| 19   | 149.5                          | 14.4                    | NKGA_PANTR           |
| 20   | 148.5                          | 14.3                    | RHCA_AGRKH           |
| 21   | 148.5                          | 14.3                    | MMGL_RAT             |
| 22   | 143.5                          | 13.9                    | NKGA_MACMU           |
| 23   | 142.5                          | 13.8                    | NKGA_HUMAN           |
| 24   | 142.5                          | 13.8                    | CD72_HUMAN           |
| 25   | 140.5                          | 13.6                    | CVXB_CRODU           |
| 26   | 140.5                          | 13.6                    | NKGC_PANTR           |
| 27   | 140.5                          | 13.6                    | LCEC_HUMAN           |
| 28   | 139.5                          | 13.5                    | LY75_HUMAN           |
| 29   | 133.9                          | 13.4                    | CD69_HUMAN           |
| 30   | 133.9                          | 13.4                    | LECH_RAT             |
| 31   | 136.5                          | 13.2                    | V008_FOWPV           |
| 32   | 136.5                          | 13.2                    | LECH_CHICK           |
| 33   | 134.5                          | 13.0                    | NKGCB_MACMU          |
|  |                                |                         | Q9mzk6 macaca mula   |
|  |                                |                         | P21715 homo sapien   |
|  |                                |                         | P21854 homo sapien   |
|  |                                |                         | Q93427 crotalus du   |
|  |                                |                         | Q9mge8 pan troglod   |
|  |                                |                         | P07307 homo sapien   |
|  |                                |                         | P07337 agkistrodon   |
|  |                                |                         | P49301 rattus norv   |
|  |                                |                         | Q9mzj3 macaca mula   |
|  |                                |                         | P26718 homo sapien   |
|  |                                |                         | Q13241 homo sapien   |
|  |                                |                         | Q9mza1 pan troglod   |
|  |                                |                         | P49300 mus musculus  |
|  |                                |                         | P14371 fowlpox vir   |
|  |                                |                         | P37217 mus musculus  |
|  |                                |                         | P34927 mus musculus  |
|  |                                |                         | Q92478 homo sapien   |
|  |                                |                         | Q95m4 pan troglod    |
|  |                                |                         | P07306 rattus norv   |
|  |                                |                         | P07337 agkistrodon   |
|  |                                |                         | P49301 rattus norv   |
|  |                                |                         | Q9mzj3 macaca mula   |
|  |                                |                         | P26715 homo sapien   |
|  |                                |                         | P21854 homo sapien   |
|  |                                |                         | Q93427 crotalus du   |
|  |                                |                         | Q9mge8 pan troglod   |
|  |                                |                         | P07307 homo sapien   |
|  |                                |                         | P07337 agkistrodon   |
|  |                                |                         | P49301 rattus norv   |
|  |                                |                         | Q07344 homo sapien   |
|  |                                |                         | P02706 rattus norv   |
|  |                                |                         | P14370 fowlpox vir   |
|  |                                |                         | P02707 gallus gallus |
|  |                                |                         | Q9mzk6 macaca mula   |

|    |  |                  |
|----|--|------------------|
| RC | TISSUE=Pancreas;   | PubMed=22388257; |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Shernman C.M., Schuler G.D., Krausser R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altschuler S.P., Zeeberg B.R., Buetow K.H., Max S.I., Wang J.J., Hsieh F., Hopkins R.F., Jordan H., Moore T., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Stapleton M., Soares M.B., Bonaldo M.F., Casarotto T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshikai K.S., Carninci P., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzyz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences;" |                  |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).   |                  |
| CC | -!- FUNCTION: Involved in lymphocyte proliferation and functions as a signal transducing receptor in lymphocytes, natural killer (NK) cells, and platelets.  |                  |
| CC | -!- SUBUNIT: Homodimer; disulfide-linked.  |                  |
| CC | -!- TISSUE SPECIFICITY: Expressed on the surface of activated T-cells, B-cells, natural killer cells, eosinophils, epidermal, Langhans cells and Platelets.  |                  |
| CC | -!- DEVELOPMENTAL STAGE: Earliest inducible cell surface glycoprotein acquired during lymphoid activation.   |                  |
| CC | -!- INDUCTION: By antigens, mitogens or activators of PKC on the surface of T and B lymphocytes. By interaction of IL-2 with the p55 IL-2R on the surface of NK cells.   |                  |
| CC | -!- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE THYMOCYTES AND ACTIVATED T LYMPHOCYTES  |                  |
| CC | -!- SIMILARITY: Contains 1 C-type lectin family domain.  |                  |
| CC | -!- DATABASE: NAME=PROW; NOTE=CD guide cd69 entry. WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd69.htm".   |                  |
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| CC | DR EMBL; L07555; ARB46359_1; -.  |                  |
| DR | EMBL; 222576; CAA80298_1; -.   |                  |
| DR | EMBL; Z30426; CAA83017_1; -.   |                  |
| DR | EMBL; Z30410; CAA83017_1; JOINED.  |                  |
| DR | EMBL; Z30427; CAA83017_1; JOINED.  |                  |
| DR | EMBL; Z30429; CAA83017_1; JOINED.  |                  |
| DR | EMBL; Z30428; CAA83017_1; JOINED.  |                  |
| DR | EMBL; BC007037; AAH07037_1; -.   |                  |
| DR | PIR; JH0822; JH0822.   |                  |
| DR | PDB; 1E87; 18-JUL-03.  |                  |
| DR | PDB; 1E81; 18-JUL-03.  |                  |
| DR | Genew; HGNC:1694; CD69.  |                  |
| DR | MIM; 107273; -.  |                  |
| DR | GO; GO:0005887; C:integral to plasma membrane; TAS.  |                  |
| DR | F:transmembrane receptor activity; TAS.  |                  |
| DR | InterPro; IPR001304; Lectin_C.   |                  |
| DR | Pfam; PF0059; Lectin_c_1.  |                  |
| DR | SMART; SM0034; CLECT_1.  |                  |
| DR | PROSITE; PS00615; C_TYPELECTIN_1; FALSE_NEG.   |                  |
| DR | PROSITE; PS50041; C_TYPELECTIN_2_1.  |                  |
| KW | Antigen; Signal-anchor; Transmembrane; Lectin; Glycoprotein; Phosphorylation; 3D-structure.  |                  |
| FT | DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).   |                  |
| FT | TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  |                  |

DR MGI:107540; Kirbla.  
 DR InterPro; IPR002333; AntifreezeII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_C\_1.  
 DR PRINTS; PR00356; ANTIFREEZEII.  
 SMART; SM00034; CLECT\_1.  
 PROSITE; PS00615; C TYPE LECTIN\_1; FALSE\_NEG.  
 PROSITE; PS50041; C TYPE LECTIN\_2\_1.  
 Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 DOMAIN 1 42 CYTOSMIC (POTENTIAL).  
 TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 210 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 39 39 S->I (IN REF. 2).  
 SEQUENCE 227 AA; 2569 MW; 0599A2557DF0B615 CRC64;

Query Match 16.7%; Score 172.5; DB 1; Length 227;  
 Best Local Similarity 24.4%; Pred. No. 7.9e-10;  
 Matches 53; Conservative 35; Mismatches 86; Indels 43; Gaps 8;

Qy 6 IYSTDELPAAPRQDDDSRKKV-----KAVLHRPCSYLVMATGLLTIVLMSTL 54  
 Db 6 VYFGLKPPRTGPGAWHESSPSLPPDACPRLRSRSLKLSAGLILV---VILLGMSTL 61

Qy 55 -----LYORTLICCGSKXGFMCQSQRCPNLMRNGSHCYFSMEKRDNNS 99  
 Db 62 VRVLIQKPSPEKCYLQNL--NKTIDDSAKLECPQDWLSDRDCFVSVQNTWEKG 118

Qy 100 LKFCADKGSHLTFPDNGYNLFQEYVGDF--YWIGLR----DIDGMRWEDGPALS-- 150  
 Db 119 LVDCDGKGATMLIQDQEELRFLLDSIKERKNSFWIGLRTLPDMN-WKWWGSTLNSDV 177

Qy 151 LSILISNSVVQKCGTHRGGHASSEVALWICKEVL 187  
 Db 178 LKITEDTENDSCAAISGDKVTFESCNDSNRWICQKEL 214

RESULT 3  
 NK12 MOUSE STANDARD; PRT; 223 AA.  
 ID NK12 MOUSE STANDARD; PRT; 223 AA.  
 AC P27812; DT 01-AUG-1992 (Rel. 23, Created)  
 "Mouse NKR-P1. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";  
 RT 28-FEB-2003 (Rel. 41, Last sequence update)  
 RL J. Immunol. 147:1701-1708(1991).  
 RN [2]  
 SEQUENCE OF 1-29 FROM N\_A.  
 MEDLINE=92388663; PubMed=1517565;  
 RA Giorda R., Weisberg E.P., Ip T.K., Trucco M.;  
 "Genomic structure and specific expression of the natural killer cell receptor NKR-P1.";  
 RT J. Immunol. 149:1957-1963(1992).  
 CC -|- FUNCTION: May function as signal-transmitting receptor.  
 CC -|- SUBCELLULAR LOCATION: Type II membrane protein.

-|- TISSUE SPECIFICITY: Natural killer cells.  
 -|- SIMILARITY: Contains 1 C-type lectin family domain.

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CC DR EMBL; W77677; AAA39823.1; -;  
 CC DR EMBL; X64721; CAA5974.1; -;  
 CC DR PTR; B4467; B4467.  
 MGD; MGI:107539; Klrblb.  
 DR InterPro; IPR002353; AntifreezeII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR PF00059; lectin\_C\_1.  
 DR PRINTS; PR00356; ANTIFREEZEII.  
 SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2\_1.  
 Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 FT TRANSMEM 1 43 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 4 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 64 223 C-TYPE LECTIN (LONG FORM).  
 FT DOMAIN 93 212 BY SIMILARITY.  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 223 AA; 25157 MW; 8D04C11DEBA9C56 CRC64;

Query Match 16.1%; Score 167; DB 1; Length 223;  
 Best Local Similarity 23.3%; Pred. No. 2.7e-09; Gaps 8;

Qy 6 IYSTDELPAAPRQDDDSRKKV-----RWKVAVLHRPCPVSY-----LYMVALGH 46  
 Db 7 VIADDNLNARIQEPKHDSPPSLSPDCCRCPRW-----HHLALKFGAGLILLVIVVIGC 60

Qy 47 TVILMSLLYQRTLCCG-----SKGEMQSQCSCPQNLWWRNGSHCYFSMEKDWNSSIK 101  
 Db 61 VLVLISVQKSSVQKL-CADYQENRNTTDCSVLNLCFQVSNLVEEGQA 120

Qy 102 FCADKGSHLTFPDNGYNLFQEVWGEDE-YWTGLR----DDGWRWEDGPALS--LS 152  
 Db 121 DCGRKGATLILQIQQEFLPFLSFKERYKNSFWIGLRFPLDMN-WKWTNGTTPNSDVK 179

Qy 153 ILSNNSVVQKCGTHRGGHASSEVALWICKEVL 187  
 Db 180 ITGDTTENGSCASISGDKVTSESCTDNRMICQREL 214

RESULT 4  
 CD94 MACMU STANDARD; PRT; 179 AA.  
 ID CD94 MACMU AC Q9MKZ9; Q9GK91; Q9MZK8;  
 "Mouse NKR-P1. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";  
 RT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).  
 DE KLRL1 OR CD94 GN Macaca mulatta (Rhesus macaque).  
 OC Fukuyrta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Macaca. [1]  
 OC Cercopitheciinae; Cercopithecidae; NCBI\_TaxID=9544; OX RN

|   |  |  |
|---|--|--|
| SEQUENCE FROM N.A. (ISOFORM 1; 2 AND 3). MEDLINE=20322487; PubMed=10866118;   | Db   | 56 SDCCSCHERKWWGYRNCYTTSEEKTNESRNRHFCASOKSSLLQNRDLEDFMSS--SOH 113  |
| LaBonte M.L., Levy D.B., Letvin N.L.; "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D."; Immunogenetics 51:496-499 (2000).   | Qy   | 130 FYWIGL--RDIDGWRWEDGPALSILNSVVK--CGTIRHG-LHASSCEVALQW 182   |
| [2] SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=21158386; PubMed=11261935;  | Db   | 114 FYWIGLSISSEHTAWLWNGSALSQYLFFETPKPRNIAINSKGNALDECTKNRYI 173   |
| Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua.";  | Qy   | [2]  |
| Immunogenetics 53:69-73(2001).  | Db   | 183 CEKVIL 187   |
| -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.   | Qy   | 174 CKQQL 178  |
| -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family members.  | RN   |  |
| -!- SUBCELLULAR LOCATION: Type II membrane protein.   | RN   |  |
| -!- ALTERNATIVE PRODUCTS:   | RN   |  |
| Event=Alternative splicing; Named isoforms=3;   | RN   |  |
| Name=1; Synonyms=CD94-A;  | RN   |  |
| Isold=Q0M2K9-1; Sequence=Displayed;   | RN   |  |
| Name=2; Synonyms=CD94-B;  | RN   |  |
| Isold=Q0M2K9-2; Sequence=VSP_003055;  | RN   |  |
| Name=3; Synonyms=CD94 alt;  | RN   |  |
| Isold=Q0M2K9-3; Sequence=VSP_003054;  | RN   |  |
| -!- TISSUE SPECIFICITY: Natural killer cells.   | RN   |  |
| -!- SIMILARITY: Contains 1 C-type lectin family domain.   | RN   |  |
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| -----   | RN   |  |
| EMBL; AF19031; AAFT4527..1;   | Db   | SEQUENCE FROM N.A. MEDLINE=87250656; PubMed=3597443;   |
| EMBL; AF190932; AAFT4528..1;  | Db   | RA Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,  |
| EMBL; AF190933; AAFT4529..1;  | Db   | RA Loeb J.A., Holland E.C., Drickamer K.,  |
| EMBL; AF234887; 1EGG.   | Db   | RT "Major and minor forms of the rat liver asialoglycoprotein receptor are independent galactose-binding proteins. Primary structure and glycosylation heterogeneity of minor receptor forms.";  |
| HSSP; P22897; 1EGG.   | Db   | RT [2]   |
| InterPro: IPR001304; Lectin_C.  | Db   | RN SEQUENCE FROM N.A. MEDLINE=87250656; PubMed=3597443;  |
| Pfam; PF00059; lectin_c_1.  | Db   | RA Halberg D.F., Wager R.E., Farrell D.C., Hildreth J., Quesenberry M.S.,  |
| SMART; SM00034; CLECT_1.  | Db   | RA Loeb J.A., Holland E.C., Drickamer K.,  |
| PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.   | Db   | RT "Primary structure of the rat liver asialoglycoprotein receptor is similar to that of the mouse receptor.";   |
| PROSITE: PS05041; C_TYPE_LECTIN_2; 1.   | Db   | RT Sanford J.P., Elliott R.W., Doyle D.,   |
| Antigen; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.  | Db   | RT "Asialoglycoprotein receptor genes are linked on chromosome 11 in the mouse.";  |
| DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  | Db   | RL J. Biol. Chem. 262:9828-9838(1987).   |
| TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  | Db   | RN J. Biol. Chem. 259:770-778(1984).   |
| -----   | RN   | RT "Mediates the endocytosis of plasma glycoproteins to which the terminal sialic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes terminal galactose and N-acetylglucosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand are dissociated. The receptor then returns to the cell membrane surface."; |
| DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).  | Db   | CC SEQUENCE OF 201-301. MEDLINE=14111554; PubMed=6319386;  |
| FT C-TYPE LECTIN (LONG FORM).   | Db   | RA Drickamer K., Mamon J.F., Binns G., Leung J.O.;   |
| DOMAIN 98 176 BY SIMILARITY.  | Db   | RT "Primary structure of the rat liver asialoglycoprotein receptor.  |
| DISULFID 61 72 BY SIMILARITY.   | Db   | RT STRUCTURAL EVIDENCE FOR THE RAT LIVER ASIALOGLYCOPROTEIN RECEPTOR.  |
| DISULFID 89 174 BY SIMILARITY.  | Db   | RT "Major and minor forms of the rat liver asialoglycoprotein receptor are independent galactose-binding proteins.";   |
| DISULFID 152 166 BY SIMILARITY.   | Db   | RT [3]   |
| CARBONYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  | Db   | RN SEQUENCE FROM N.A. MEDLINE=89170119; PubMed=3234178;  |
| CARBONYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  | Db   | RA SEQUENCE FROM N.A. MEDLINE=89170119; PubMed=3234178;  |
| VARSPLIC 1 34 MAVFTTFLRISGTGLGICLSMTAGLTLKNS -> MAA (in isoform 3).   | Db   | RA "Primary structure of the rat liver asialoglycoprotein receptor.  |
| VARSPLIC 105 105 L -> LQ (in isoform 2).  | Db   | RT "The receptor is internalized and transported to a sorting organelle, where receptor and ligand are dissociated. The receptor then returns to the cell membrane surface.";  |
| VARIANT 139 139 Y -> D.   | Db   | CC SEQUENCE OF 201-301. MEDLINE=14111554; PubMed=6319386;  |
| SEQUENCE 179 AA; 20607 MW; 06212B4494527F07 CRC64;  | Db   | RA Drickamer K., Mamon J.F., Binns G., Leung J.O.;   |
| Query Match 15..8%; Score 16..5; DB 1; Length 179;  | Db   | RT "Primary structure of the rat liver asialoglycoprotein receptor.  |
| Best Local Similarity 31..2%; Pred. No. 4..7e-09;   | Db   | RT STRUCTURAL EVIDENCE FOR THE RAT LIVER ASIALOGLYCOPROTEIN RECEPTOR.  |
| Matches 39; Conservative 19; Mismatches 58; Indels 9; Gaps 4;   | Db   | RT "Major and minor forms of the rat liver asialoglycoprotein receptor are independent galactose-binding proteins.";   |
| -----   | CC -!- SUBCELLULAR LOCATION: Type II membrane protein.   |  |
| CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal cells.  | CC -!- MISCELLANEOUS: Calcium is required for ligand binding.  |  |
| CC -!- MISCELLANEOUS: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1.  | CC -!- MISCELLANEOUS: Two types of rat hepatic lectin differ in their carbohydrate structures.                                     |  |
| CC -!- MISCELLANEOUS: RHL-2 and RHL-3 only differs in their carbohydrate structures.  | CC -!- MISCELLANEOUS: Two types of rat hepatic lectin have been identified, RHL-1 and RHL-2/3, having a relative abundance of 4:1. |  |
| 70 SQCSRCPNPNWNRNGSHCYFSMEKDWNSSLKFCADGGSHLLTPDNNOGVNLFOBYVGED 129  | QY   |  |

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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CC EMBL; M16347; AAA4038\_1; -;

DR EMBL; J02762; AAA41522\_1; -;

DR EMBL; X07633; CAA30476\_1; -;

PIR; B24462; LNRT2;

HSnr; P06734; IHL1;

InterPro; IPR002333; AntifreezeII.

DR InterPro; IPR001304; Lectin\_C.

DR InterPro; IPR00564; Lectin\_N.

Pfam; PF00059; lectin\_c\_1.

DR Pfam; PF03954; lectin\_N\_1.

DR SMART; SN00034; ANTIFREEZEII.

DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; 1.

DR PROSITE; PS50041; C\_TYPELECTIN\_2; 1.

KW Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane;

KW Calcium; Signal-anchor; Phosphorylation.

FT DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 80 301 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 169 295 C-TYPE LECTIN (LONG FORM).

FT DISULFID 170 181 BY SIMILARITY.

FT DISULFID 198 285 BY SIMILARITY.

FT DISULFID 271 285 BY SIMILARITY.

FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .).

FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .).

FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .).

FT CONFLICT 153 153 R -> A (IN REF. 1).

FT CONFLICT 202 202 R -> N (IN REF. 2 AND 3).

FT CONFLICT 260 260 C -> W (IN REF. 2 AND 3).

SEQUENCE 301 AA; 34943 MW; 3C2315E642D71279 CRC64;

Query Match 15.6%; Score 161.5; DB 1; Length 301;

Best Local Similarity 27.3%; Pred. No. 1.3e-08;

Matches 39; Conservative 22; Mismatches 67; Indels 15; Gaps 3;

QY 5B RTLCGGSKGFMCSQCSRCPNLMWRGTSCTTFSMEKRDWNSSLKPCADKGSHLLTFPDHQ 117

Db 153 RTLTQQLAFFLNGTBCCPWNVEFGSCTWFSRGLTWAEDQYCQMELAHLLIVINSB 212

QY 118 GVNLQEVVYSEDFYVIGLRLDGD-WRWEQDPAISLISNSVWQ --- KCG 163

Db 213 EQEFTVKHRAFHITGLTDKGSKWDOGTTEYRSNFKWAFTQPDNCQHEEGGSEDDCA 272

QY 164 TIIHRCGL-HASSCEVALQWCEK 185

Db 273 EILSDCLWINDFCQQNRWACER 295

Query Match 15.4%; Score 159.5; DB 1; Length 220;

Best Local Similarity 25.3%; Pred. No. 1.5e-08;

Matches 46; Conservative 33; Mismatches 74; Indels 29; Gaps 8;

QY 27 KAVIHLRPCVSYLVNVAYGLITVILMSLY-----QRLGCCSKGEMGSQCSR----- 74

Db 38 RLALKLSCAGLILIV----LTLIGMSVLVRYQPSREKCC---VFLQENLNKTIVNLE 90

QY 75 CPNUKMRNSHCYFFSMERKDWNSSLLKEADKGSHLLTFPDNGCVNLFBYVGEDF--YW 132

Db 91 CPQWLHDKCFVYSQVNTWEEQDQGRKATLJJQDQBRFLFEDSIVKYNFW 150

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Natural killer cell surface protein P1-40 (NKR-P1 40) (NKR-P1.9).

GN KLRRB1C OR LY55C OR LY55-C.

OS Mus musculus (Mouse).

OC Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

|                       |  |   |         |
|-----------------------|--|---|---------|
| QY                    | 145  | DGPALS--LSTLNSNTVQKCGTIIHRGGLHASCEVALQWICRKVL | 187     |
| ID                    | NK13_RAT   | STANDARD;                                     | PRT;    |
| ID                    | P27471;  |   | 223 AA. |
| AC                    | DT 01-AUG-1992 (Rel. 23, Created)<br>DT 01-AUG-1992 (Rel. 23, Last sequence update)<br>DT 15-MAR-2004 (Rel. 43, Last annotation update)  |   |         |
| DE                    | Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen<br>3.2.3).  |   |         |
| OS                    | Rattus norvegicus (Rat).   |   |         |
| OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  |   |         |
| OC                    | NCBI_TaxID=10161;  |   |         |
| RN                    |  |   |         |
| RP                    | SEQUENCE FROM N.A. PubMed=2399464;   |   |         |
| RX                    | MEDLINE=9037805; PubMed=2399464;   |   |         |
| RA                    | Giorida R., Rudert W.H., Vavassori C., Chambers W.H., Hiserodt J.C., Trucco M.,  |   |         |
| RT                    | "NKR-P1, a signal transduction molecule on natural killer cells."  |   |         |
| RL                    | Science, 249:1198-1200(1990).  |   |         |
| CC                    | -!- FUNCTION: Mediates transmembrane signaling in natural killer (NK) cells and so may act as a receptor able to selectively trigger NK cell activity.   |   |         |
| CC                    | -!- SUBCELLULAR LOCATION: Type II membrane protein.  |   |         |
| CC                    | -!- TISSUE SPECIFICITY: Natural killer cells.  |   |         |
| CC                    | -!- MISCELLANEOUS: Ligand binding may be calcium dependent.  |   |         |
| CC                    | -!- SIMILARITY: Contains 1 C-type lectin domain.   |   |         |
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| EMBL                  | MG62891; AAA41710.1; -.  |   |         |
| PIR                   | A35917; A35917.  |   |         |
| HSPE                  | P22897; 1EGG.  |   |         |
| DR                    | InterPro; IPR001304; Lectin_C.   |   |         |
| DR                    | Pfam; PF0059; lectin_c_1.  |   |         |
| DR                    | PRINTS; PR00356; ANTIFREEZEII.   |   |         |
| DR                    | SMART; SMO034; CLCT.   |   |         |
| DR                    | PROSITE; PS00615; C_TYPELECTIN_1; FALSE_NEG.   |   |         |
| DR                    | PROSITE; PS50041; C_TYPELECTIN_2; 1.   |   |         |
| DR                    | Glycoprotein; Antigen; Transmembrane; Signal_anchor; Lectin.   |   |         |
| FT                    | DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).   |   |         |
| FT                    | TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  |   |         |
| FT                    | DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).   |   |         |
| FT                    | DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).   |   |         |
| FT                    | DISULFID 94 102 BY SIMILARITY.   |   |         |
| FT                    | DISULFID 122 210 BY SIMILARITY.  |   |         |
| FT                    | DISULFID 189 202 BY SIMILARITY.  |   |         |
| FT                    | CARBOHYD 82 82 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| FT                    | CARBOHYD 143 143 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| FT                    | CARBOHYD 169 169 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| SQ                    | SEQUENCE 223 AA; 24551 MW; FCD12B12DDF4330 CRC64;  |   |         |
| Query Match           | 15.4%; Score 159.5%; DB 1; Length 223;   |   |         |
| Best Local Similarity | 23.5%; Pred. No. 1.5e-0; Mismatches 33; Indels 21; Gaps 5;   |   |         |
| Matches               | 39; Conservative   |   |         |
| CC                    | 38 IMMUNOGLOBULINS-----LILYQRTLCCCSQSCSPNMRNSHCVF  | 89  |         |
| CC                    | 54 LALVGMISLYRVLYQKPSVCPVLIQENIISKTPAKL---KCPKDWLSHRDCKPHV   | 108   |         |
| CC                    | 90 SMEKRDWNSSKTFADKGSHLTFDNGQYNLFQEYVG--EDFYWIGLR--DIDGMRWE  | 144   |         |
| CC                    | 109 SQTGTTWKESLLADCGKGATLILVQDEELFRNLTRISSEFQIGSYTSLDSENWKW  | 168   |         |
| CC                    | RESULT 7   |   |         |
| CC                    | NK13_RAT   |   |         |
| CC                    | P27471;  |   |         |
| CC                    | DT 01-AUG-1992 (Rel. 23, Created)  |   |         |
| CC                    | DT 01-AUG-1992 (Rel. 23, Last sequence update)   |   |         |
| CC                    | DT 15-MAR-2004 (Rel. 43, Last annotation update)   |   |         |
| CC                    | DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen<br>3.2.3).   |   |         |
| CC                    | OS Rattus norvegicus (Rat).  |   |         |
| CC                    | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus   |   |         |
| CC                    | OC NCBI_TaxID=10161;   |   |         |
| CC                    | RN   |   |         |
| CC                    | RP SEQUENCE FROM N.A. PubMed=2399464;  |   |         |
| CC                    | RX MEDLINE=9037805; PubMed=2399464;  |   |         |
| CC                    | RA Giorida R., Rudert W.H., Vavassori C., Chambers W.H., Hiserodt J.C., Trucco M.,   |   |         |
| CC                    | RT "NKR-P1, a signal transduction molecule on natural killer cells."   |   |         |
| CC                    | RL Science, 249:1198-1200(1990).   |   |         |
| CC                    | CC -!- FUNCTION: Mediates transmembrane signaling in natural killer (NK) cells and so may act as a receptor able to selectively trigger NK cell activity.  |   |         |
| CC                    | CC -!- SUBCELLULAR LOCATION: Type II membrane protein.   |   |         |
| CC                    | CC -!- TISSUE SPECIFICITY: Natural killer cells.   |   |         |
| CC                    | CC -!- MISCELLANEOUS: Ligand binding may be calcium dependent.   |   |         |
| CC                    | CC -!- SIMILARITY: Contains 1 C-type lectin domain.  |   |         |
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| CC                    | CC EMBL; MG62891; AAA41710.1; -.   |   |         |
| CC                    | CC PIR; A35917.  |   |         |
| CC                    | CC HSPE; P22897; 1EGG.   |   |         |
| CC                    | CC DR InterPro; IPR002353; AntifreezeII.   |   |         |
| CC                    | CC DR Pfam; PF0059; lectin_c_1.  |   |         |
| CC                    | CC DR PRINTS; PR00356; ANTIFREEZEII.   |   |         |
| CC                    | CC DR SMART; SMO034; CLCT.   |   |         |
| CC                    | CC DR PROSITE; PS00615; C_TYPELECTIN_1; FALSE_NEG.   |   |         |
| CC                    | CC DR PROSITE; PS50041; C_TYPELECTIN_2; 1.   |   |         |
| CC                    | CC DR Glycoprotein; Antigen; Transmembrane; Signal_anchor; Lectin.   |   |         |
| CC                    | CC FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).   |   |         |
| CC                    | CC FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  |   |         |
| CC                    | CC FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).   |   |         |
| CC                    | CC FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).   |   |         |
| CC                    | CC FT DISULFID 94 102 BY SIMILARITY.   |   |         |
| CC                    | CC FT DISULFID 122 210 BY SIMILARITY.  |   |         |
| CC                    | CC FT DISULFID 189 202 BY SIMILARITY.  |   |         |
| CC                    | CC FT CARBOHYD 82 82 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| CC                    | CC FT CARBOHYD 143 143 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| CC                    | CC FT CARBOHYD 169 169 N-LINKED (GLCNAC. . . ) (POTENTIAL).  |   |         |
| CC                    | CC SQ SEQUENCE 223 AA; 24551 MW; FCD12B12DDF4330 CRC64;  |   |         |
| CC                    | CC Query Match 15.4%; Score 159.5%; DB 1; Length 223;  |   |         |
| CC                    | CC Best Local Similarity 23.5%; Pred. No. 1.5e-0; Mismatches 33; Indels 21; Gaps 5;  |   |         |
| CC                    | CC Matches 39; Conservative  |   |         |
| CC                    | CC 38 IMMUNOGLOBULINS-----LILYQRTLCCCSQSCSPNMRNSHCVF   | 89  |         |
| CC                    | CC 54 LALVGMISLYRVLYQKPSVCPVLIQENIISKTPAKL---KCPKDWLSHRDCKPHV  | 108   |         |
| CC                    | CC 90 SMEKRDWNSSKTFADKGSHLTFDNGQYNLFQEYVG--EDFYWIGLR--DIDGMRWE   | 144   |         |
| CC                    | CC 109 SQTGTTWKESLLADCGKGATLILVQDEELFRNLTRISSEFQIGSYTSLDSENWKW   | 168   |         |
| CC                    | CC RESULT 8  |   |         |
| CC                    | CC DECI MOUSE STANDARD;  |   |         |
| CC                    | CC ID LECI MOUSE STANDARD;   |   |         |
| CC                    | CC AC P24721;  |   |         |
| CC                    | CC DT 01-MAR-1992 (Rel. 21, Created)   |   |         |
| CC                    | CC DT 01-MAR-1992 (Rel. 21, Last sequence update)  |   |         |
| CC                    | CC DT 15-MAR-2004 (Rel. 43, Last annotation update)  |   |         |
| CC                    | CC DE Asialectoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R)   |   |         |
| CC                    | CC DE (ASGP-R)   |   |         |
| CC                    | CC GN ASGR2 OR ASGR-2  |   |         |
| CC                    | CC OS Mus musculus (Mouse)   |   |         |
| CC                    | CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  |   |         |
| CC                    | CC OC NCBI_TaxID=10096;  |   |         |
| CC                    | CC RN  |   |         |
| CC                    | CC RP SEQUENCE FROM N.A.   |   |         |
| CC                    | CC RA STRAIN=C57BL/6; TISSUE=Liver;  |   |         |
| CC                    | CC RX MEDLINE=91027942; PubMed=2223888;  |   |         |
| CC                    | CC RA Sanford J.P., Doyle D.J.,  |   |         |
| CC                    | CC RA "Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes during mammalian evolution."  |   |         |
| CC                    | CC RA Biophys. Acta 1087:259-261(1990).  |   |         |
| CC                    | CC [1]   |   |         |
| CC                    | CC RN  |   |         |
| CC                    | CC SEQUENCE FROM N.A.  |   |         |
| CC                    | CC RX STRAIN=FB/N; TISSUE=Liver;   |   |         |
| CC                    | CC RX MEDLINE=22388257; PubMed=12477932;   |   |         |
| CC                    | CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Derge J.,   |   |         |
| CC                    | CC RA Klausner R.D., Wagner L., Schuler C.M., Schuler C.,  |   |         |
| CC                    | CC RA Altschul S.F., Zeeberg B., Bustadt K.H., Schaefer C.F., Bhat N.K.,   |   |         |
| CC                    | CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  |   |         |
| CC                    | CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.,  |   |         |
| CC                    | CC RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  |   |         |
| CC                    | CC RA Raha S.S., McEvany P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Mullaly S., Loqueland J., Kettman M., Abramson M., Abra   |   |         |
| CC                    | CC RA Bosak S.A., Peters M., Abramson M., Kettman M., Hale S., Garcia A.M., Madan A., Rodriguez S., Rodriguez Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimmow J.W., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schniech A., Schein J.E., Jones S.J.M., Marra M.A./  |   |         |
| CC                    | CC RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Rodriguez S., Sanchez R.A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rutherford Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,   |   |         |
| CC                    | CC RA Schniech A., Schein J.E., Jones S.J.M., Marra M.A./  |   |         |
| CC                    | CC RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."   |   |         |
| CC                    | CC RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  |   |         |
| CC                    | CC CC FUNCTION: Mediates the endocytosis of plasma glycoproteins to which the terminal sialic acid residue on their complex carbohydrate moieties has been removed. The receptor recognizes the terminal galactose and N-acetylgalactosamine units. After ligand binding to the receptor, the resulting complex is internalized and transported to a sorting organelle, where receptor and ligand disasociated. The receptor then returns to the cell membrane surface.  |   |         |
| CC                    | CC CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  |   |         |
| CC                    | CC CC -!- TISSUE SPECIFICITY: Expressed exclusively in hepatic parenchymal cells.  |   |         |
| CC                    | CC CC -!- MISCELLANEOUS: Calcium is required for ligand binding.   |   |         |
| CC                    | CC CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  |   |         |
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|      |   |   |  |
|------|---|---|--|
| RX   | MEDLINE=98350122; PubMed=9683661;   | DR  | GO; GO:0007165; P:signal transduction; TAS.  |
| RA   | Glinek J., Sobanov Y., Brostic C., Steffens C., Nguyen C., Lehrach H., Hofer E., Francis F., and D receptor genes in the human natural killer gene complex.";   | DR  | InterPro; IPR002353; AntirezeelI.  |
| RT   | "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex."   | DR  | InterPro; IPR001304; Lectin_C.   |
| RL   | Immogenetics 48:163-173 (1998).   | DR  | Pfam; PF00059; Lectin_C_1.   |
| RN   | [3]   | DR  | PRINTS; PRO0356; ANTIREZEELI.  |
| RN   | SEQUENCE FROM N.A.  | DR  | SMART; SM00034; CLECT1; 1.   |
| RA   | Kothapalli R., Kusmartsseva I., Loughran T.P. Jr.; "Identification and characterization of the NKG2D gene from large granular lymphocytic leukemia (LGL) cells.";   | DR  | PROSITE; PS00615; C-TYPE LECTIN_1; FALSE NEG.  |
| RT   | Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases  | DR  | PROSITE; PS50041; C-TYPE LECTIN_2; 1.  |
| RN   | [4]   | FT  | PROTEIN; PS00615; C-TYPE LECTIN_2; 1.  |
| RN   | SEQUENCE FROM N.A., AND VARIANT THR-72.   | FT  | KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein; Polymorphism; 3D-structure.   |
| XX   | MEDLINE=21623889; PubMed=1751968;   | FT  | FT CYTOPLASMIC (POTENTIAL).  |
| RA   | Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guechlein L.A., Uhrlberg M., Parham P.;  | FT  | FT TRANSMEM SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  |
| RT   | "Conservation and variation in human and common chimpanzee CD94 and NKG2 genes".  | FT  | FT DOMAIN EXTRACELLULAR (POTENTIAL).   |
| RL   | J. Immunol. 168:240-252 (2002).   | FT  | FT DOMAIN C-TYPE LECTIN (LONG FORM).   |
| RN   | [5]   | FT  | FT DISULFID BY SIMILARITY.   |
| RA   | SEQUENCE FROM N.A.  | FT  | FT DISULFID BY SIMILARITY.   |
| XX   | TISSUE=Testis;  | FT  | FT DISULFID BY SIMILARITY.   |
| XX   | MEDLINE=22388257; PubMed=12477932;  | FT  | FT DOMAIN N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| RA   | Straubinger R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaerer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heieh F., Atchachenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEvlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | FT  | FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).  |
| RT   | RT  | FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL). |  |
| RN   | RT  | FT VARIANT A->T (in allele NKG2-D*02).          |  |
| RA   | SEQUENCE FROM N.A.  | FT  | FT SEQUENCE /FTId=YAR 013295.  |
| XX   | TISSUE=Testis;  | FT  | FT SEQUENCE C22FBDB533D7800E CRC64;  |
| XX   | MEDLINE=22388257; PubMed=12477932;  | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| RA   | Straubinger R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaerer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heieh F., Atchachenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEvlan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| CC   | -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-B molecules by NK cells and some cytotoxic T-cells.   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| CC   | -!- SUBUNIT: Can form disulfide-bonded heterodimer with CD94.   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| CC   | -!- SUBCELLULAR LOCATION: Type II membrane protein.   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| CC   | -!- TISSUE SPECIFICITY: Natural killer cells.   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| CC   | -!- SIMILARITY: Contains 1 C-type lectin family domain.   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
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| CC   | -----   | FT  | FT SEQUENCE 25274 MW: C22FBDB533D7800E CRC64;  |
| DR   | X54870; CPA38652_1; -.  | RC  | TISSUE=Blood;  |
| EMBL | X54870; CPA38652_1; -.  | RC  | MEDLINE=96011B48; PubMed=7589107;  |
| DR   | AJ001687; CAA04925_1; -.  | RX  | Chang C., Rodriguez A., Carretero M., Lopez-Bonet M., Phillips J.H., Lanier L.L., "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; |
| EMBL | AJ001687; CAA04925_1; JOINED.   | RA  | Eur. J. Immunol. 25:2433-2437(1995).   |
| DR   | AAL6181; AAF86573_1; -.   | RT  | [2]  |
| EMBL | AAL6181; AAF86573_1; -.   | RN  | SEQUENCE FROM N.A.   |
| DR   | AF260135; AAF86573_1; -.  | RC  | TISSUE=Placent;  |
| EMBL | AF260135; AAF86573_1; -.  | RC  | MEDLINE=98139529; PubMed=947066;   |
| DR   | BC039836; AAH39836_1; -.  | RX  | Rodriguez A., Carretero M., Glienke J., Belion T., Ramirez A., Lebrach H., Francis F., Lopez-Bonet M., "Structure of the human CD94 C-type lectin gene.";  |
| DR   | PIR; PT0375; PT0375.  | RA  | Immunogenetics 47:305-309(1998).   |
| PDB  | 1HYR; 23-MAY-01.  | RT  | IMMUNOGENETICS 47:305-309(1998).   |
| DR   | IYCG; 09-JAN-02.  | RL  | IMMUNOGENETICS 47:305-309(1998).   |
| GO   | GO:0005887; C:integral to plasma membrane; TAS.   | RA  | Lebrach H., Francis F., Lopez-Bonet M., "Structure of the human CD94 C-type lectin gene.";   |
| DR   | GO:0004872; F:receptor activity; TAS.   | RT  | Immunogenetics 47:305-309(1998).   |
| DR   | GO:0006960; P:antimicrobial humoral response (sensu Inver. . . ; TAS.   | RL  | IMMUNOGENETICS 47:305-309(1998).   |





|                       |            |   |                  |         |
|-----------------------|------------|---|------------------|---------|
| Qy                    | 130        | FWYIGHLDIDG-WRWEDECPLSISLNSNVQ-   | KCGTIIHRCG-LHASS | 174     |
| Db                    | 228        | VSWIGLTDQNPWRWVAPLQDNNWFHGGLGGGEDCAHITGGRWNDDV  | 287              |         |
| Qy                    | 175        | CEVALQWICERKV1  | :                | 187     |
| Db                    | 288        | CQRTERWICEMKL   | 300              |         |
| RESULT 14             |            |   |                  |         |
| V239_POMPV            | V239_POMPV | STANDARD;   | PRT;             | 163 AA. |
| ID                    | ID         |   |                  |         |
| AC                    | AC         |   |                  |         |
| DT                    | DT         | 01-JAN-1990 (Rel. 13, Created)  |                  |         |
| DT                    | DT         | 16-OCT-2001 (Rel. 40, Last sequence update)   |                  |         |
| DT                    | DT         | 16-OCT-2001 (Rel. 40, Last annotation update)   |                  |         |
| DE                    | DE         | Putative C-type lectin protein FPV239 (BamHI-ORF8).   |                  |         |
| DN                    | DN         | FPV239.   |                  |         |
| OS                    | OS         | Foot-and-mouth disease virus (PPV).   |                  |         |
| OC                    | OC         | Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;   |                  |         |
| OC                    | OC         | Avipoxvirus.  |                  |         |
| OX                    | OX         | NCBI_TaxID=10261;   |                  |         |
| RN                    | RN         | [1]   |                  |         |
| RP                    | RP         | SEQUENCE FROM N.A.  |                  |         |
| RX                    | RX         | MEDLINE=20193820; PubMed=10729156;  |                  |         |
| RA                    | RA         | Alfonso C.L., Tuiman E.R., Lu Z., Zsak L., Kitish G.F., Rock D.H.;  |                  |         |
| RT                    | RT         | "The genome of the foot-and-mouth disease virus.";  |                  |         |
| RL                    | RL         | J. Virol. 74:3815-3831(2000).   |                  |         |
| RN                    | RN         | [2]   |                  |         |
| RP                    | RP         | SEQUENCE OF 1-116 FROM N.A.   |                  |         |
| RC                    | RC         | STRAIN=FP-9 / Isolate HP-438;   |                  |         |
| RX                    | RX         | Medline=882293622; Pubmed=2836548;  |                  |         |
| RA                    | RA         | Tomley F., Bins M., Campbell J., Boursnell M.E.G.;  |                  |         |
| RT                    | RT         | "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of foot-and-mouth disease virus."   |                  |         |
| RT                    | RT         | J. Gen. Virol. 67:1025-1040(1988).  |                  |         |
| CC                    | CC         | - - SIMILARITY: Contains 1 C-type lectin family domain.   |                  |         |
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| CC                    | CC         | DR EMBL; AF198100; AAF44533_1; -.   |                  |         |
| DR                    | DR         | D00295; BA00203_1; -.   |                  |         |
| DR                    | DR         | PIR; H29963; MWYZ88.  |                  |         |
| DR                    | DR         | HSPP; P05140; 2A9P.   |                  |         |
| DR                    | DR         | InterPro; IPR01304; Lectin_C.   |                  |         |
| DR                    | DR         | Pfam; PF00059; lectin_Q; 1.   |                  |         |
| DR                    | DR         | SMART; SM00034; CLECT1.   |                  |         |
| DR                    | DR         | PROSITE; PS00615; C_TYPELECTIN_1; FALSE_NEG.  |                  |         |
| DR                    | DR         | PROSITE; PS50041; C_TYPELECTIN_2; 1.  |                  |         |
| KW                    | KW         | Hypothetical protein; Lectin.   |                  |         |
| FT                    | FT         | DOMAIN 48 159 C-TYPE LECTIN.  |                  |         |
| SEQUENCE              | SEQUENCE   | 163 AA; 18635 MW; 5156DC892885532 CRC64;  |                  |         |
| SQ                    | SQ         |   |                  |         |
| Query Match           | 14.9%      | Score 154; DB 1; Length 163;  |                  |         |
| Best Local Similarity | 22.9%      | Pred. No. 3.7e-08;  |                  |         |
| Matches               | 38;        | Conservative 31; Mismatches 65; Indels 32; Gaps 5;  |                  |         |
| Qy                    | 33         | PCVSVLVMAQLLTIVLMS-----LILYQRTLCCGSKGFMQSQCSCPNCMWMRNGS   | 84               |         |
| Db                    | 18         | PCGS--IIIIVSVFTILSTRPPVPPDIXLY-----CKEGTVGYNK 57  |                  |         |
| Qy                    | 85         | HCYFVSEKMRDKWNSLKFCDAKGKSHLLTFPDNOGYNLFQHYVGEDFYWIGLRDID--GW 141  |                  |         |
| Db                    | 58         | NCYFFSEEKNKSLAVERCKMDGELTSISKEEBKFILRYKGPNRHWIGLEKVDENGTV 117   |                  |         |
| Qy                    | 142        | PWFDGDAY STI SNTSYOKCCTEBCI HASSCVYALWTCRKYT  | 187              |         |

|                       |   |                                     |
|-----------------------|---|-------------------------------------|
| Query                 | Match   | 14.9%; Score 154; DB 1; Length 199; |
| Best Local Similarity | 22.7%; Pred. No.  | 4.6e-08;                            |
| Matches               | 35; Conservative  | 32; Mismatches                      |
| Qy                    | 45 LLTVMLLQLYRQITLCCGSKGFMC-----                                      | -SQCSRCPNLWNRNGSHCYXFSEMEK 93       |
| Ddb                   | 46 LIVVLITSLLITALIANTVNGK - YNCGLYKELESSDHVATCKNEWLYSKRTCFSTTT 103    |                                     |
| Qy                    | 94 RDWNNSSLKFCADKGSHLLTDPDNOGNLHQEYVGDEFYIWIGRLD - LDGWRNEDGPAISL 151 |                                     |
| Ddb                   | 104 KSWALAQRSCESDAAATAVIDSEKDWTFLKRSGELEHWHIGLRNEANOTKWANGKEFN- 162   |                                     |
| Qy                    | 152 S1LNNSVQRCGTTIHRGHLASSCVELQWICEK 185                              |                                     |
| Ddb                   | 153 SWENITSGSRSVNRKNTAVDCEANFHWSK 196                                 |                                     |
| Qy                    | 154 SWEFNTSGSRSVNRKNTAVDCEANFHWSK 196                                 |                                     |

| Result No. | Score | Query | Match | Length | DB     | ID  | Description  |
|------------|-------|-------|-------|--------|--------|---|--|
| <hr/>      |       |       |       |        |        |   |  |
| -          | 1     | 103.6 | 100.0 | 188    | 11     | Q64335  | rattus norvegicus (Rattus norvegicus) C-type lectin, 1; another C-type lectin, 1; signal transduction molecule on mast cells is secreted |
| 2          | 83.8  | 60.9  | 188   | 11     | Q88713 | Q64335 rattus norvegicus (Rattus norvegicus) C-type lectin, 1; another C-type lectin, 1; signal transduction molecule on mast cells is secreted |  |
| 3          | 545.5 | 52.7  | 189   | 4      | Q75613 | Q88713 mus musculus   |  |
| 4          | 541.5 | 52.3  | 195   | 4      | Q96E93 | Q75613 homo sapiens   |  |
| 5          | 525.5 | 50.7  | 189   | 4      | Q43198 | Q96E93 homo sapiens   |  |
| 6          | 201.5 | 19.4  | 275   | 11     | Q9D403 | Q43198 homo sapiens   |  |
| 7          | 184   | 17.8  | 257   | 13     | Q90636 | Q9D403 mus musculus   |  |
| 8          | 178   | 17.2  | 181   | 4      | Q9NZS2 | Q90636 gallus gallus  |  |
| 9          | 178   | 17.2  | 231   | 4      | Q9NZS2 | Q90636 gallus gallus  |  |
| 10         | 177.5 | 17.1  | 200   | 13     | Q80288 | Q90636 gallus gallus  |  |
| 11         | 177   | 17.1  | 231   | 6      | Q8MI05 | Q90636 gallus gallus  |  |
| 12         | 177   | 17.1  | 238   | 11     | QBBR04 | Q90636 gallus gallus  |  |
| 13         | 176.5 | 17.0  | 422   | 6      | Q8HY11 | Q90636 gallus gallus  |  |
| 14         | 175   | 16.9  | 179   | 11     | Q54708 | Q90636 gallus gallus  |  |
| 15         | 175   | 16.9  | 179   | 11     | Q54707 | Q90636 gallus gallus  |  |
| 16         | 174.5 | 16.8  | 171   | 4      | Q9UHP7 | Q90636 gallus gallus  |  |

|  |  |                   |         |             |  |  |  |
|--|--|-------------------|---------|-------------|--|--|--|
| Query Match  | 100.0%   | Score 1036;       | DB 11;  | Length 188; |  | Qy   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |
| Best Local Similarity  | 100.0%   | Pred. No. 1e-102; |         |             |  | Db   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |
| Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   |  |                   |         |             |  |  |  |
|  |  |                   |         |             |  |  |  |
| Qy   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |                   |         |             |  | Qy   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |
| Db   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |                   |         |             |  | Db   | 1 MADNSIYSTLELPAAPIVQDDSRWKYKAVLHRPCVSYLVMVVALGLITVIMSLLYORTL 60   |
|  |  |                   |         |             |  |  |  |
| Qy   | 61 CGGSKGFMCSQCSRCPNLWMRNGSHCYXFSMEKRDNNSSLKFCADKGSHLITFPDNGVN 120 |                   |         |             |  | Qy   | 61 CGGSKGFMCSQCSRCPNLWMRNGSHCYXFSMEKRDNNSSLKFCADKGSHLITFPDNGVN 120 |
| Db   | 61 CGGSKGFMCSQCSRCPNLWMRNGSHCYXFSMEKRDNNSSLKFCADKGSHLITFPDNGVN 120 |                   |         |             |  | Db   | 61 CGGSKGFMCSQCSRCPNLWMRNGSHCYXFSMEKRDNNSSLKFCADKGSHLITFPDNGVN 120 |
|  |  |                   |         |             |  |  |  |
| Qy   | 121 LFQEYVGEDFWIGLRIDGWRWEDGPAISLSILSNVVQKCGTIIHRCGLIASCEVALQ 180  |                   |         |             |  | Qy   | 121 LFQEYVGEDFWIGLRIDGWRWEDGPAISLSILSNVVQKCGTIIHRCGLIASCEVALQ 180  |
| Db   | 121 LFQEYVGEDFWIGLRIDGWRWEDGPAISLSILSNVVQKCGTIIHRCGLIASCEVALQ 180  |                   |         |             |  | Db   | 121 LFQEYVGEDFWIGLRIDGWRWEDGPAISLSILSNVVQKCGTIIHRCGLIASCEVALQ 180  |
|  |  |                   |         |             |  |  |  |
| Qy   | 181 WICEKVLP 188   |                   |         |             |  | Qy   | 181 WICEKVLP 187   |
| Db   | 181 WICEKVLP 188   |                   |         |             |  | Db   | 181 WICEKVLP 187   |
|  |  |                   |         |             |  |  |  |
| RESULT 2   |  |                   |         |             |  | RESULT 3   |  |
| Q88713   | PRELIMINARY;   | PRT;              | 188 AA. |             |  | 075613   | PRELIMINARY;   |
| ID Q88713;   |  |                   |         |             |  | ID 075613;   |  |
| AC Q88713;   |  |                   |         |             |  | AC 075613;   |  |
| DT 01-NOV-1998 (TREMBLrel. 08, Created)  |  |                   |         |             |  | DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)   |  |
| DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)   |  |                   |         |             |  | DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)   |  |
| DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)   |  |                   |         |             |  | DE ITIM-containing receptor MAFA-L.  |  |
| DT Mammal cell Function-associated antigen 2F1 (MAFA) (killer cell lectin-like receptor GI).   |  |                   |         |             |  | GN MAFA.   |  |
| DN KLRG1 OR MAFA.  |  |                   |         |             |  | OS Homo sapiens (Human).   |  |
| OC Mus musculus (Mouse).   |  |                   |         |             |  | OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.         |  |
| OC Eukaryota; Metacozia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus                          |  |                   |         |             |  | OC   |  |
| OX NCBI_TaxID=10090;   |  |                   |         |             |  | RN NCBI_TaxID=9606;  |  |
| RN [1]   |  |                   |         |             |  | RN [1]   |  |
| SEQUENCE FROM N.A.   |  |                   |         |             |  | RP SEQUENCE FROM N.A.  |  |
| RE STRAIN=C.B-17 SCID;   |  |                   |         |             |  | RP Butcher S., Arney K.L., Cook G.P.;  |  |
| RE MEDLINE=90077194; PubMed=9862378;   |  |                   |         |             |  | RP "MAFA-L, an ITIM-containing receptor encoded by the human NK cell gene complex and expressed by basophils and NK cells."; |  |
| RE Hanke T., Corral L., Vance R.E., Raulet D.H.;   |  |                   |         |             |  | RP RT Eur. J. Immunol. 28:0-1(1998).   |  |
| RT "2F1 antigen, the mouse homolog of the rat 'SI', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";                 |  |                   |         |             |  | RL DR EMBL; AF097358; AAC2200.1; -.  |  |
| RT Eur. J. Immunol. 28:4409-4417(1998).  |  |                   |         |             |  | DR EMBL; AF097358; AAC2200.1; -.   |  |
| RP SEQUENCE OF 2-188 FROM N.A.   |  |                   |         |             |  | DR GO; GO-000529; F:sugar binding; IEA.  |  |
| RA Blaser C.;  |  |                   |         |             |  | DR InterPro; IPR001304; Lectin C.  |  |
| RA Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases   |  |                   |         |             |  | DR Pfam; PF00059; Lectin C.  |  |
| RN [3]   |  |                   |         |             |  | DR SMART; SM00034; CLECT_C_1.  |  |
| SEQUENCE FROM N.A.   |  |                   |         |             |  | DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   |  |
| RE STRAIN=L29/SverTACFB <sub>r</sub> ; TISSUE=Spleen;  |  |                   |         |             |  | SQ SEQUENCE 189 AA; 21206 MW; FA9023FL123656A8 CRC64;  |  |
| RE MEDLINE=21115136; PubMed=11220622;  |  |                   |         |             |  | Query Match 52.7%; Score 545.5%; DB 4; Length 189;   |  |
| RA "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLrg1), the mouse homologue of MAPA." |  |                   |         |             |  | Best Local Similarity 55.1%; Pred. No. 3.1e-50;  |  |
| RA Immungenerics 52:206-211(2001).   |  |                   |         |             |  | Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;   |  |
| DR EMBL; AF097357; AAC0318.1; -.   |  |                   |         |             |  |  |  |
| DR EMBL; AF09751; AAC03342.1; -.   |  |                   |         |             |  |  |  |
| DR MGD; MGI:1552941; Kirg1.  |  |                   |         |             |  |  |  |
| DR GO; GO:0004872; F:receptor activity; IEA.   |  |                   |         |             |  |  |  |
| DR GO; GO:0005529; F:sugar binding; IEA.   |  |                   |         |             |  |  |  |
| DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.  |  |                   |         |             |  |  |  |
| DR InterPro; IPR001304; Lectin C.  |  |                   |         |             |  |  |  |
| DR Pfam; PF00059; Lectin C.  |  |                   |         |             |  |  |  |
| DR SMART; SM00034; CLECT_C_1.  |  |                   |         |             |  |  |  |
| DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   |  |                   |         |             |  |  |  |
| KW Lectin Receptor   |  |                   |         |             |  |  |  |
| SEQUENCE 188 AA;   |  |                   |         |             |  |  |  |
| Query Match 80.9%; Score 838; DB 11; Length 188;   |  |                   |         |             |  |  |  |
| Best Local Similarity 80.7%; Pred. No. 1.e-81;   |  |                   |         |             |  |  |  |
| Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;   |  |                   |         |             |  |  |  |



|                       |  |   |   |
|-----------------------|--|---|---|
| DR                    | MGD; MGI:1918433; 4933425B16Rik.   | Qy  | 93 KRDWNSSLKFCADKGSHLLTPDNQGVNLFOEYVGDFYWGGLRIDLG---WRWEDGPAL 149   |
| DR                    | GO; GO:00529; F:sugar binding; IEA.  | Db  | 147 ESDWNSSREHCHRLGASLATDKEEMEFM/QQRPADRWLGHRAEGDEHWTWADGSAF 206  |
| DR                    | Intero; IPR001304; Lectin_C.   |   |   |
| DR                    | Pfam; PF00059; Lectin_C_1.   |   |   |
| DR                    | SMART; SM00034; CLECT_1.   |   |   |
| DR                    | PROSTTE; PS50041; C_TYPE_LECTIN 2; 14.   | Qy  | 150 SLSILSNSVQV --- KCGTHRHCGHLHASCEVALWICKEK 185   |
| SQ                    | SEQUENCE 275 AA; 31360 MW; C9792BA25C8B5CC2 CRC64;                                 | Db  | 207 T---NRPVFELGGRCAYLNDDGISSALCHSEKFWVCSR 243  |
| Query Match           | 19.4%; Score 201.5; DB 11; Length 275;   |   |   |
| Best Local Similarity | 23.4%; Pred. No. 3.1e-13;  |   |   |
| Matches               | 63; Conservative 40; Mismatches 77; Indels 89; Gaps 11;                            | RESULT 8  |   |
| Qy                    | 1 MADNSTTSLLEPAAPVQ-----DSSRWKVAVLHRPCVSYLVNVAGLG 45                               | ID Q9NZS1   | PRELIMINARY; PRT; 181 AA.   |
| Db                    | 1 MSDEVFTATIQLQDSAVRGNDGNURKEPHPAQSLLWRGAAL---SLLMLCIVLYTGL 57                     | AC  |   |
| Qy                    | 46 LTIVLM-----SLLY 56  | DT  | 01-OCT-2000 (TrEMBLrel. 15, Created)  |
| Db                    | 58 VTLATMFLQVNSDINSDEKLSQLQKSIIHPQODNLSELSNSRKSLSQTSQTSALLE 117                    | DT  | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)   |
| Qy                    | 57 OR---TLCGGSKGFMC----SQCSRCPNLWMRNGSHCYFSM-EKRDWNSSLKFCADKG 107                  | DE  | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)   |
| Db                    | 118 RQBQMAPKLC -- KEFLHASDHIKCNPPKTIWQYGNSSCYYSINEERKWSPSRKDCIDRN 175              | GN  | Lectin-like receptor F1, splice variant 1 KLRF1-s1.   |
| Qy                    | 108 SHLITPFDNQGVNLFOEYVG- EDFYVIGLR DIDG-WRWEDEGPALSLSLISNSVY--- 159               | OS  | Homo sapiens (Human)  |
| Db                    | 176 ATLVKIDSTDELLQSLTSFESPFGLGSWNSGRNMWEDGSPFPPTLSDKELASF 235                      | OC  | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
| Qy                    | 160 --QKCCTIHRGHLHASCEVALWICKEK 185  | OC  | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |
| Db                    | 236 NGSRRECAYFERNIYTSCRRAEIPWICKEK 264   | RN  |   |
| RESULT 7              |  | SEQUENCE FROM N.A.  |   |
| Q90636                | PRELIMINARY; PRT; 257 AA.  | RX  | MDLNLNE=20135860; PubMed=10671213   |
| AC                    |  | RA  | Roda-Navarro P.; Arce I.; Reneo M.; Montgomery K.; Kucherlapati R.,   |
| Q90636;               |  | RA  | Fernandez-Ruiz E.;  |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Created)   | RT  | "Human KLRF1, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis."; |
| DT                    | 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)                                  | RT  |   |
| DB                    | 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)                                | RT  |   |
| GN                    | 17.5.  | DR  | Bur. J. Immunol. 30:568-576 (2000).   |
| OS                    | Gallus gallus (Chicken)  | DR  | EMBL: AF175207; AACF7805.1; -   |
| OC                    | Archaeauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;              | DR  | GO; GO:001620; C:membrane; TAS.   |
| OC                    | Gallus.  | DR  | GO; GO:0030106; F:MHc class I receptor activity; TAS.   |
| CX                    | NCBItaxID=9031;  | DR  | InterPro: IPR001304; Lectin_C.  |
| RN                    | [1]  | DR  | Pfam; PF00059; Lectin_C_1.  |
| RP                    | SEQUENCE FROM N.A.   | DR  | SMART; SM00034; CLECT_1.  |
| RC                    | TISSUE=Spleen.   | DR  | PROSITE: PS50041; C_TYPE_LECTIN_2.  |
| XX                    | MEDLINE=9416491; PubMed=8119728;   | KW  | Receptor.   |
| FA                    | Bernot A., Zoorab R., Aufriay C.;  | SEQUENCE  | 181 AA; 21204 MW; 64642240GAE1E551 CRC64;   |
| RT                    | "Linkage of a new member of the lectin supergene family to the chicken Mhc genes." | Matches   | 51; Conservative 32; Mismatches 77; Indels 44; Gaps 9;  |
| RL                    | Immunogenetics 39:221-229 (1994).  | Qy  | 1 MADNSLYSTELPLAAPRVRQ-DDSRKVK---AVLHRPCVSYLVNVAL---GLITVILM 51   |
| EMBL                  | PIR: 150146; IS0146.   | Db  | 1 MQDERYMTLNQSKKRSSAQTSQLFKDYSVTLH---WYKILLGIGSTVNGILTTLI 56  |
| DR                    | DR   | 52 SLLYORTLCGGSKGFMCSCORCPNLPWNRNGSHCYFSMEKRDWNSSLKFCADKGSHLL 111 |   |
| DR                    | DR   | 57 SLIL-----LVLCOSEWLKYQGKCYWFNSMRSNSDSVYCLERKSHLL 100            |   |
| DR                    | DR   | Qy  | 58 MLLYORTLCGGSKGFMCSCORCPNLPWNRNGSHCYFSMEKRDWNSSLKFCADKGSHLL 111   |
| DR                    | DR   | Db  | 112 TFPDNGQVNLFQEYVGE-DFYWGGLRIDL---GWRWEDGPALSLSL---SNSVVQ 160   |
| DR                    | DR   | 101 LHDQLEMAFTQNRQLNFTYKMTWWVDGSPIDSCKFFTKGPARKERS--- 157         |   |
| DR                    | DR   | Qy  | 161 KCGTHRHCGHLHASCEVALWICKEK 184   |
| DR                    | DR   | Db  | 158 -CAAIKESKIFSETSSVFRWICQ 180   |
| DR                    | PRINTS; PR003556; ANTIFREEZEII.  | RESULT 9  |   |
| DR                    | SMART; SM00034; CLECT_1.   | ID Q9NZS2   | PRELIMINARY; PRT; 231 AA.   |
| DR                    | PROSITE; PS50041; C_TYPE_LECTIN_2; 1.  | AC  |   |
| SQ                    | SEQUENCE 257 AA; 28814 MW; C672B483F4E85333 CRC64;                                 | DT  | 01-OCT-2000 (TrEMBLrel. 15, Created)  |
| Query Match           | 17.8%; Score 184; DB 13; Length 257;   | DT  | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)   |
| Best Local Similarity | 28.6%; Pred. No. 2.2e-11;  | DT  | 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)   |
| Matches               | 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;                             | DE  | Lectin-like receptor F1 (Activating coreceptor NKp80).  |
| Qy                    | 33 PCVSYLVMVAGLTLVIMSLLYORTLCGGSKGFMCSCORCPNLPWNRNGSHCYFSME 92                     | GN  | KLRF1 OR MD/LR/KLRF1.   |
| Db                    | 101 PC----MLVIALVAVL-----QRFSCSRPRPF---SHVCNPNAWVGFGKCYFSDF 146                    | OS  | Homo sapiens (Human).   |





"Cloning of a mouse homolog of CD94 extends the family of C-type lectins on murine natural killer cells.";  
 RT Bar, J., Immuno. 27:3236-3241(1997).  
 RT EMBL; AF030122; AAC28244.1; -.  
 DR MGD; MGII:11162757; Klrd1.  
 GO; GO:0005529; F-sugar binding; IEA.  
 InterPro; IPR006204; EGF-like.  
 InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00041; lectin\_C\_1.  
 SMART; SM00034; CLECT; 1.  
 PROSITE; PSS00041; C\_TYPE\_LCTIN\_2; 1.  
 PROSITE; PS000022; EGF\_1; 1.  
 SEQUENCE 179 AA; MW; D59E1CBB63139B45 CRC64;

Query Match 16.9%; Score 175; DB 11; Length 179;  
 Best Local Similarity 27.9%; Pred. No. 1..3e-10;  
 Matches 50; Conservative 36; Mismatches 71; Indels 22; Gaps 10;  
 Qy 22 SRWKVKAHR-PCVSILVVALGLITYLMSLLYQTLTC-GGSKGPM-CGSGCRPNL 78  
 DR 7 TRWLMSTVFGLKCL--FLMVTIGVLLNSTFIQNSTPSPTTVEQEVSSECVCILDK 64  
 Qy 79 WMENGSHCYXFSMKRDWNSSLKPCADKSHLITFPDNGVNLFQEQYEDFYWIGL-- 135  
 DR 65 WVGHQCNCPFISKEEKSWKRSRDFCASNSSLQ-PQRNELSMNNF-SQTFFWIGHYS 122  
 Qy 136 RDIDGWRWEDGPALSLSLN-SVYQKCGTIHRC----GLHASCEVALQWICRYV 186  
 DR 123 EKRNALWEDGTVPSKDLIPEFSVIRP---EHCVVSPSKSVSAESCNKRYICKL 177

Search completed: August 10, 2004, 16:18:50  
 Job time : 33.6089 secs

## RESULT 15

054707 PRELIMINARY; PRT; 179 AA.

AC 054707; (TREMBrel. 06, Created)  
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)  
 DT 01-JUN-1998 (TREMBrel. 25, Last annotation update)  
 DE Killer cell lectin-like receptor, subfamily D, member 1 (CD94).  
 GN KLRL OR CD94.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Heusel J.W., Ho E.L., Brown M.G., Mattsumoto K., Yokoyama W.M.;  
 RL "Murine CD94.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 27:0-0(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE-Mammary gland,  
 RA Butcher S., Cottage A., Cook G.P.;  
 RT "Mouse natural killer cell receptors homologous to human CD94 and  
 RT NK2-D.";  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF030311; AAC28243.1; -.  
 DR EMBL; AF057714; AAC33713.1; -.  
 DR BMBI; AF039025; AD02116.1; -.  
 DR MGD; MGII:11196275; Klrd1.  
 DR GO; GO:0005529; F-sugar binding; IEA.  
 GO; GO:0007157; P-heterophosphorylation; IEA.  
 InterPro; IPR001304; EGF like.  
 DR InterPro; IPR006209; EGF like.  
 DR SMART; SM00034; CLECT; 1.  
 PROSITE; PS50041; C\_TYPE\_LCTIN\_2; 1.

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|  |                 |               |            |                    |                     |                    |
|--|-----------------|---------------|------------|--------------------|---------------------|--------------------|
| Gencore version 5.1.6<br>(c) 1993 - 2004 Compugen Ltd.   | 26              | 179.5         | 17.3       | 295                | 6                   | ABR43189 Human REM |
| Copyright  | 27              | 177.5         | 17.1       | 229                | 3                   | AAY6765 Membrane-  |
| OM protein - protein search, using sw model.   | 28              | 177.5         | 17.1       | 229                | 4                   | AAT11432 Human PRO |
| Run on:  | 29              | 177.5         | 17.1       | 229                | 4                   | AAB65288 Human PRO |
| Title: US-09-811-367B-5  | 30              | 177.5         | 17.1       | 229                | 5                   | ABP43587 Membrane  |
| Perfect score: 1036  | 31              | 177.5         | 17.1       | 229                | 6                   | ABU59103 Human PRO |
| Sequence: 1 MADNSIYSTLELPAAPRQD.....GLHASSCEYALQWICKEVKVLP 188   | 32              | 177.5         | 17.1       | 229                | 6                   | ABU59181 Novel hum |
| Scoring table: BLOSUM62  | 33              | 177.5         | 17.1       | 229                | 6                   | ABU62693 Human sec |
| Gapext 10.0 , Gapext 0.5   | 34              | 177.5         | 17.1       | 229                | 6                   | ABO1776 Novel hum  |
| Searched: 1586107 seqs, 28547505 residues  | 35              | 177.5         | 17.1       | 229                | 6                   | ABU6012 Human sec  |
| Total number of hits satisfying chosen parameters: 1586107   | 36              | 177.5         | 17.1       | 229                | 6                   | ABU13994 Human PRO |
| Minimum DB seq length: 0   | 37              | 177.5         | 17.1       | 229                | 6                   | ABU81130 Human sec |
| Maximum DB seq length: 2000000000  | 38              | 177.5         | 17.1       | 229                | 6                   | ABU72579 Novel hum |
| Post-processing: Minimum Match 0%  | 39              | 177.5         | 17.1       | 229                | 6                   | ABU6830 Human sec  |
| Listing first 45 summaries   | 40              | 177.5         | 17.1       | 229                | 6                   | ABR39424 Human GEN |
| Database : A_Geneseq_29Jan04:*   | 41              | 177.5         | 17.1       | 229                | 6                   | ABU59911 Novel sec |
| 1: geneseqp1980s:*   | 42              | 177.5         | 17.1       | 229                | 6                   | ABU59328 Human PRO |
| 2: geneseqp2000s:*   | 43              | 177.5         | 17.1       | 229                | 6                   | ABO26025 Human sec |
| 3: geneseqp2001s:*   | 44              | 177.5         | 17.1       | 229                | 6                   | ABO25101 Human sec |
| 4: geneseqp2002s:*   | 45              | 177.5         | 17.1       | 229                | 6                   | ABU59034 Human sec |
| ALIGNMENTS   |                 |               |            |                    |                     |                    |
| RESULT 1   |                 |               |            |                    |                     |                    |
| ID AAR77033  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| AC AAR77033;   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| DT 01-FEB-1996   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| DE (first entry)   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| Mammalian mast cell function-associated antigen (MATA).  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| KW Mast cell function-associated antigen; MATA; soluble; ligand; identification; screening; inflammation; inflammatory; allergy; allergic; prevention. | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| Rattus rattus.   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| OS OS  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| PN WO9527734-A1.   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| PD 19-OCT-1995.  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| PP 06-APR-1995;  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| PR 08-APR-1994;  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| (YEDA ) YEDA RES & DEV CO LTD.   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| (RYCUS A. (RYCUS A.  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| Pecht I, Guthmann MD, Tal M;   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| WPI,1995-366356/47.  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| N-PDB; AAT01471.   | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| Claim 12; Page 37; Sipp; English.  | XX              | XX            | XX         | XX                 | XX                  | XX                 |
| SUMMARIES  |                 |               |            |                    |                     |                    |
| Result No.   | Score           | Query Match   | Length     | DB ID              | Description         |                    |
| -  | -               | -             | -          | -                  | -                   | -                  |
| 1  | 1036            | 100.0         | 188        | 2 AAR77033         | Aar77033 Mammalian  |                    |
| 2  | 1036            | 100.0         | 188        | 2 AAW88277         | Aaw88277 Rat mast   |                    |
| 3  | 1036            | 100.0         | 188        | 4 AAE11761         | Aae11761 Rat mast   |                    |
| 4  | 838             | 80.9          | 188        | 4 AAE11760         | Aae11760 Mouse mast |                    |
| 5  | 651             | 62.8          | 114        | 2 AAR77412         | Aar77412 Partial s  |                    |
| 6  | 545.5           | 52.7          | 189        | 2 ADD25635         | Add25635 Binding d  |                    |
| 7  | 525.5           | 50.7          | 189        | 2 AAW88265         | Aaw88265 Human mas  |                    |
| 8  | 525.5           | 50.7          | 189        | 4 AAE11759         | Aae11759 Human mas  |                    |
| 9  | 418.5           | 40.4          | 843        | 4 ARG05451         | Abg05451 Novel hum  |                    |
| 10   | 251.5           | 24.3          | 191        | 6 ABJ37898         | Abj37898 NOVX Prot  |                    |
| 11   | 20.0            | 99            | 2 AAW88267 | Aaw88267 Human MAF |                     |                    |
| 12   | 184.5           | 17.8          | 199        | 2 AAR54559         | Aar54559 Human CD6  |                    |
| 13   | 184.5           | 17.8          | 199        | 2 AAW88593         | Aaw88593 Human CD6  |                    |
| 14   | 184.5           | 17.8          | 199        | 7 ADD25621         | Add25621 Binding d  |                    |
| 15   | 184             | 17.8          | 257        | 2 AAW88594         | Aaw88594 Chicken 1  |                    |
| 16   | 183             | 17.7          | 228        | 4 AAU02495         | Aau02495 Human sec  |                    |
| 17   | 182             | 17.6          | 268        | 6 ABJ19338         | Abj19338 NOVX Rela  |                    |
| 18   | 182             | 17.6          | 276        | 6 ABR43190         | Abr43190 Human REM  |                    |
| 19   | 182             | 17.6          | 276        | 6 AAE37769         | Aae37769 Human C-t  |                    |
| 20   | 180             | 17.4          | 231        | 5 ABB1897          | Abb1897 Human NKP   |                    |
| 21   | 179.5           | 17.3          | 241        | 7 ADE07884         | Ade07884 Novel pro  |                    |
| 22   | 179.5           | 17.3          | 265        | 4 AAU19657         | Aau19657 Human nov  |                    |
| 23   | 179.5           | 17.3          | 265        | 5 ABP47877         | Abp47877 Human pol  |                    |
| 24   | 179.5           | 17.3          | 265        | 7 ADC10839         | Adc10839 Human ext  |                    |
| 25   | 179.5           | 17.3          | 275        | 6 ABJ19327         | Abj19327 NOVX rela  |                    |
| Query Match  | 100.0%          | Score 1036;   | DB 2;      | Length 188;        |                     |                    |
| Best Local Similarity  | 100.0%          | Prede. No. 1  | 8e-96;     | Indels 0;          | Gaps 0;             |                    |
| Matches 188;   | Conservative 0; | Mismatches 0; |            |                    |                     |                    |

Query Match    100.0%; Score 1036; DB 2; Length 188;  
 Best Local Similarity 100.0%; Pid. No. 1.8e-96;  
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MADNSIYSTLELPAAPIVQDDSRWKRKAVLHRCVSTIVMVAIGLILVILMSLLLYCRTL 60  
 Db 1 MADNSIYSTLELPAAPIVQDDSRWKRKAVLHRCVSTIVMVAIGLILVILMSLLLYCRTL 60

QY 61 CCGSKGFMCSQCSRCPNLUWRNGSHCYFSMEKRDWNSSLKECADKGSHLITFPDNGVN 120  
 Db 61 CCGSKGFMCSQCSRCPNLUWRNGSHCYFSMEKRDWNSSLKECADKGSHLITFPDNGVN 120

QY 121 LFOBYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLASSCEVALQ 180  
 Db 121 LFOBYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLASSCEVALQ 180

QY 181 WICEKVLP 188  
 Db 181 WICEKVLP 188

RESULT 2  
 ID AAW88277 standard; protein; 188 AA.  
 AC AAE11761  
 XX DT 29-MAR-1999 (first entry)  
 DE Rat mast cell function-associated antigen (MAFA).  
 XX Mast cell function-associated antigen; MAFA; splice variant; rat;  
 KW inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.  
 OS Rattus sp.  
 XX Key Location/Qualifiers  
 PH Modified-site B2..84  
 FT /note= "Asn is N-glycosylated"  
 PT Modified-site 97..99  
 FT /note= "Asn is N-glycosylated"  
 XX PN WO9854209-A2.  
 PR 03-DEC-1998.  
 PA 29-MAY-1998; 98WO-GB001572.  
 XX PR 31-MAY-1997; 97GB-00011148.  
 PR (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  
 XX DR WPI; 1999-059805/05.  
 DR N-PSDB; AAV84222.  
 XX New polypeptide having a sequence corresponding to human mast cell  
 PT function-associated antigen - useful in forming and manufacturing  
 PT pharmaceutical compositions in the treatment of inflammatory and allergic  
 PT diseases, and tumour growth.  
 XX Disclosure; Fig 4; 44pp; English.

PS This is the amino acid sequence of rat mast cell function-associated  
 CC antigen (MAFA), a type II membrane glycoprotein found on mast cells and  
 CC basophils. The invention relates to cloning of the human MAFA molecule  
 CC (see AAW88205) and to the discovery of splice variants (see AAW88266-67)  
 CC of human MAFA that are not found in rat. Polypeptides and synthetic  
 CC peptides (see AAW88255-54) based on human MAFA and human truncated MAFA,  
 CC and polynucleotides encoding them, can be used in methods for the  
 CC treatment of inflammatory and allergic diseases (e.g. rheumatoid  
 CC arthritis and asthma), and tumour growth  
 XX Sequence 188 AA;

QY 1 MADNSIYSTLELPAAPIVQDDSRWKRKAVLHRCVSTIVMVAIGLILVILMSLLLYCRTL 60  
 QY 1 MADNSIYSTLELPAAPIVQDDSRWKRKAVLHRCVSTIVMVAIGLILVILMSLLLYCRTL 60  
 Db 1 MADNSIYSTLELPAAPIVQDDSRWKRKAVLHRCVSTIVMVAIGLILVILMSLLLYCRTL 60

QY 61 CCGSKGFMCSQCSRCPNLUWRNGSHCYFSMEKRDWNSSLKECADKGSHLITFPDNGVN 120  
 QY 61 CCGSKGFMCSQCSRCPNLUWRNGSHCYFSMEKRDWNSSLKECADKGSHLITFPDNGVN 120  
 Db 61 CCGSKGFMCSQCSRCPNLUWRNGSHCYFSMEKRDWNSSLKECADKGSHLITFPDNGVN 120

QY 121 LFOQEYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLHASCEVALQ 180  
 QY 121 LFOQEYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLHASCEVALQ 180  
 Db 121 LFOQEYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLHASCEVALQ 180  
 Db 121 LFOQEYVGDFYNGLRLDGMWEDGPAISLTSLSNSVQRCGTIIRCGHLHASCEVALQ 180

QY 181 WICEKVLP 188  
 QY 181 WICEKVLP 188  
 Db 181 WICEKVLP 188

RESULT 3  
 ID AAE11761 standard; protein; 188 AA.  
 XX AC AAE11761;  
 XX DT 18-DEC-2001 (first entry)  
 XX Rat mast cell function-associated antigen (MAFA) protein.  
 DE Rat; pharmaceutical composition; mast cell function associated antigen;  
 XX KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;  
 KW immunosuppressive; cytostatic.  
 XX Rattus norvegicus.  
 OS XX PN WO200170805-A2.  
 XX PD 27-SEP-2001.  
 XX PR 16-MAR-2001; 2001WO-US008596.  
 XX PR 17-MAR-2000; 2000US-0190716P.  
 XX PA (GEMI-) GEMINI SCI INC.  
 XX PI Takahashi N, Mikayama T;  
 XX DR WPI; 2001-611482/70.  
 DR N-PSDB; AAd18736.  
 XX Pharmaceutical composition for treating tumor by stimulating cytotoxic  
 PT activity of natural killer cell or T-cell, comprises an agent that binds  
 PT to mast cell function-associated antigen ligand on target cell.  
 XX Example 1; Page 19; 49pp; English.

CC The present invention relates to a pharmaceutical composition comprising  
 CC an agent which specifically binds to a mast cell function associated  
 CC antigen (MAFA) ligand on a target cell, and prevents or inhibits natural  
 CC killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA  
 CC ligand and a pharmaceutically acceptable excipient. The invention is  
 CC useful for inhibiting an NK- or T-cell-expressed cell surface MAFA  
 CC binding to a ligand on a target cell, by contacting the pharmaceutical  
 CC composition in vitro, ex vivo or in vivo by administering the composition  
 CC to the subject, to NK or T-cell or the target cell e.g. tumour cell, in  
 CC an amount sufficient to inhibit cell surface MAFA binding to the ligand  
 CC on the target cell. The agent or the composition is useful for treating a  
 CC tumour by stimulating the cytotoxic activity of an NK cell or CTL-susceptible  
 CC T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible  
 CC tumour cell. The invention is also useful for inhibiting an activity of  
 CC NK cell or a T-cell. The present sequence is rat MAFA protein



Sequence 114 AA;

Query Match 62.8%; Score 651; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.1e-58;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 CPNLWNRNGSCHCYFSMEKRDNNSLXKPCADKGSHLTFPDNGVNLFOEYEGDFWIG 134  
1 CPNLWNRNGSCHCYFSMEKRDNNSLXKPCADKGSHLTFPDNGVNLFOEYEGDFWIG 60

Db 135 LRDINGWREGPALSLSIISNSVQKCGTHRCGLHASSCEVALQTCVKLP 188  
61 LRDIDGWRWEGPALSLSIISNSVQKCGTHRCGLHASSCEVALQTCVKLP 114

Db 62 Binding domain-immunoglobulin fusion protein #95.

RESULT 6  
ADD25635 standard; Protein; 189 AA.  
ADD25635;  
AC AC  
XX XX  
DT 15-JAN-2004 (first entry)

Binding domain-immunoglobulin fusion protein-associated protein #95.

XX Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX Unidentified.

US2003118592-A1.  
IPN 26-JUN-2003.

PP 25-JUL-2002; 2002US-00207655.  
PR 17-JAN-2001; 2001US-0367358P.  
PR 17-JAN-2002; 2002US-0385530.  
PR 03-JUN-2002; 2002US-0385691P.

(GENB-) GENECRAFT INC.

PPI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;  
WPI: 2003-801317/75.

New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

Disclosure; SEQ ID NO 196; 157pp; English.

The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain polypeptide, and an immunoglobulin heavy chain constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues; an immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polynucleotide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple sclerosis or autoimmune disease. The present sequence is a binding domain -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

Sequence 189 AA;

Query Match 52.7%; Score 545.5; DB 7; Length 189;  
Best Local Similarity 55.1%; Pred. No. 7.1e-47;  
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTIELPLPAAPVQODDSRWRKAVLHRPCVSYLYVALGILTVILMSLLIVQRTL 60  
DB 1 MTDSTIYSMELPLATQAQNDYGPQOKSSSRPSCCLVIALGLITAVLSSVLLTQWL 60

QY 61 CCGSKGFGMCQSQCSCPNCPLNMRRNGSHCYFSMEKRDNNSLXKPCADKGSHLTFPDNGVNL 120  
DB 61 CGQGSNYSTCASCPSCPDRMKYGNHCFYFSEVEKDWNSSLIEFCLARDSHLIVTNDQEMS 120

QY 121 LFQBTKVGDYDYGIRDIDEWGRWEQGPAQLS-TLNSNSVYQKCGTHRCGHASSCEVAL 179  
DB 121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180

QY 180 QWICKEKV 186  
DB 181 HWVCKKV 187

RESULT 7  
AAW88265 standard; protein; 189 AA.  
ID AAW88265;  
AC AAW88265;  
XX 29-MAR-1999 (first entry)

DE Human mast cell function-associated antigen (MAFA).  
XX AAW88265  
XX Mast cell function-associated antigen; MAFA; splice variant; human;  
XX inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.  
XX Homo sapiens.

Key Location/Qualifiers  
PT 7..10 "RTIM motif"  
PT /note= "Asn is N-glycosylated"  
Modified-site 65..67 /note= "Asn is N-glycosylated"  
PT Modified-site 97..99 /note= "Asn is N-glycosylated"  
PT Modified-site 97..99 /note= "Asn is N-glycosylated"

FT Modified-site /note= "Asn is N-glycosylated" 150..152  
 FT /note= "Asn is N-glycosylated"  
 XX WO9854209-A2.  
 XX 03-DEC-1998.  
 PD 29-MAY-1998; 98WO-GB001572.  
 PF 31-MAY-1997; 97GB-00011148.  
 PR XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX PI Hewitt BL, Lamont A, Williams DH,  
 XX WPI: 1999-059806/05.  
 DR N-PSDB; AAV84198.  
 XX New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  
 Disclosure; Fig 1; 44pp; English.  
 XX This is the amino acid sequence of human mast cell function-associated antigen (MAFA), a type II membrane glycoprotein, cDNA (see AAV84198) encoding human MAFA can be obtained from myelogenous leukemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAV88277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2. Alternatively spliced forms (see AAV88266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAV88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth.  
 XX Sequence 189 AA;  
 Query Match Best Local Similarity 50.7%; Score 525.5; DB 2; Length 189;  
 Matches 100; Conservative 29; Nismatches 57; Indels 1; Gaps 1;  
 SQ Sequence 189 AA;  
 Query Match Best Local Similarity 53.5%; Score 525.5; DB 4; Length 189;  
 Matches 100; Conservative 29; Nismatches 57; Indels 1; Gaps 1;  
 SQ Sequence 189 AA;

Query Match Best Local Similarity 53.5%; Pred. No. 7.4e-45; Length 189;  
 Matches 100; Conservative 29; Nismatches 57; Indels 1; Gaps 1;  
 SQ Sequence 189 AA;

Db 1 MADNSIYSTELPAAPRVDODSRWKVAKVILHRPCYSVLMVVAIGLHTVILMSLILYQORTI 60  
 Db 1 MTDSVITYSMELPLTATQANDYGPQKSSSSKPKSSCLVLTGGLATAILSVALYQWIL 60

Qy 1 CCGSKGFMCSQCSRCPNLNMRRNGSHCYFFSMEKRDWNSSLKECADKGSHLITFPDNQGYN 120  
 Db 61 CGGSNYSTASCPSPDRMKYGNFYYVEEDWNSSLEFLARDSHLLVTDNOMS 120

Qy 61 COGSNYSTASCPSPDRMKYGNFYYVEEDWNSSLEFLARDSHLLVTDNOMS 120

Db 121 LFQEYVGEDDYWIGLIRDIDOWRWEQDGPALSLS-TLSNSTVQKCQTITHRCGLHASSCEVAL 179  
 Db 121 LLQVPLSEAFCWIGLRNNSGWRWEQDGPALSLS-TLSNSTVQKCQTITHRCGLHASSCEVAL 180

Qy 180 QWICKV 186  
 Db 181 HGvCKKV 187

RESULT 8  
 AAE11759 standard; protein; 189 AA.  
 XX AAE11759;  
 AC AAE11759;  
 DT 18-DEC-2001 (First entry)  
 XX Human mast cell function associated antigen (MAFA) protein.  
 DE Human; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CMV;  
 KW Novel human diagnostic protein #5442.

RESULT 9  
 ABG05451  
 ID ABG05451 standard; protein; 843 AA.  
 XX ABG05451;  
 AC ABG05451;  
 DT 13-FEB-2002 (first entry)  
 XX Novel human diagnostic protein #5442.

|                       |  |  |  |  |
|-----------------------|--|--|--|--|
| XX                    | Human chromosome mapping; gene mapping; gene therapy; forensics;             | XX   | AC AEJ37898;   |  |
| KW                    | food supplement; medical imaging; diagnostic; genetic disorder;              | XX   | XX DT 22-MAY-2003 (first entry)  |  |
| XX                    | Homo sapiens.  | XX   | DE NOVX protein sequence SEQ ID No 42.   |  |
| XX                    | WO200175067-A2.  | XX   | XX Hepatotropic; immunosuppressive; cardiotonic; hypertensive; tranquilizer;       |  |
| PD                    | 11-OCT-2001.   | XX   | KW vulnary; viricide; antibacterial; protozoicide; fungicide; nootropic;           |  |
| XX                    | PP 30-MAR-2001; 2001WO-US008631.   | XX   | KW antiparasitic; neuroprotective; cerebroprotective; anti-parkinsonian;           |  |
| XX                    | PR 31-MAR-2000; 2000US-00540317.   | XX   | KW anticonvulsant; anti-addictive; analgesic; dermatological; keratolytic;         |  |
| PR                    | 23-AUG-2000; 2000US-00649167.  | XX   | KW antiseborheic; antiseptic; anti-inflammatory; osteopathic;                      |  |
| XX                    | PA (HYSE-) HYSEQ INC.  | XX   | KW cytostatic; anti-laxative; anti-psoriatic; hypotensive; osteopathic;            |  |
| XX                    | Drmanac RT, Liu C, Tang YT;  | XX   | KW antiulcer; anorectic; antidiabetic; anti-allergic; haemostatic;                 |  |
| PI                    | WPI; 2001-639362/73.   | XX   | KW neuroleptic; antidepressant; antiinfertility; NOVX; human disease;              |  |
| DR                    | N-PSDB; AAS9638.   | XX   | KW parasitic infection; Alzheimer's disease; stroke; bacterial; fungal; protozoal; |  |
| XX                    | ET New isolated polynucleotide and encoded polypeptides, useful in           | XX   | KW parasitic infection; Drmanac's disease; stroke; forensic biology;               |  |
| PT                    | diagnostics, forensics, gene mapping, identification of mutations            | XX   | KW immunogen; non-human transgenic animal; gene therapy.                           |  |
| PT                    | responsible for genetic disorders or other traits and to assess              | XX   | XX Unidentified.   |  |
| PT                    | biodiversity.  | XX   | OS PN WC200281517-A2.  |  |
| XX                    | CC Claim 20; SEQ ID NO 35810; 103pp; English.                                | XX   | PR 19-JAN-2001; 2001US-0262892P.   |  |
| CC                    | CC The invention relates to isolated polynucleotide (I) and polypeptide (II) | XX   | PR 23-JAN-2001; 2001US-0263598P.   |  |
| CC                    | CC sequences. (I) is useful as hybridization probes, polymerase chain        | XX   | PR 24-JAN-2001; 2001US-0263739P.   |  |
| CC                    | CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,   | XX   | PR 25-JAN-2001; 2001US-0264117P.   |  |
| CC                    | CC and in recombinant production of (II). The polynucleotides are also used  | XX   | PR 26-JAN-2001; 2001US-0264478P.   |  |
| CC                    | CC in diagnostics as expressed sequence tags for identifying expressed       | PR 30-JAN-2001; 2001US-0263351P.   |  |  |
| CC                    | CC genes. (I) is useful in gene therapy techniques to restore normal         | PR 02-JUN-2001; 2001US-0272870P.   |  |  |
| CC                    | CC activity of (III) or to treat disease states involving (II). (II) is      | PR 14-MAR-2001; 2001US-0275927P.   |  |  |
| CC                    | CC useful for generating antibodies against it, detecting or quantitating a  | PR 14-MAR-2001; 2001US-0275990P.   |  |  |
| CC                    | CC polypeptide in tissue, as molecular weight markers and as a food          | PR 20-MAR-2001; 2001US-0276449P.   |  |  |
| CC                    | CC supplement. (III) and its binding partners are useful in medical imaging  | PR 20-MAR-2001; 2001US-0277358P.   |  |  |
| CC                    | CC of sites expressing (III). (I) and (II) are useful for treating disorders | PR 23-MAR-2001; 2001US-0278151P.   |  |  |
| CC                    | CC involving aberrant protein expression or biological activity. The         | PR 29-MAR-2001; 2001US-0279851P.   |  |  |
| CC                    | CC polypeptide and polynucleotide sequences have applications in             | PR 20-APR-2001; 2001US-0285140P.   |  |  |
| CC                    | CC diagnostics, forensics, gene mapping, identification of mutations         | PR 20-APR-2001; 2001US-0285141P.   |  |  |
| CC                    | CC responsible for genetic disorders or other traits to assess biodiversity  | PR 20-APR-2001; 2001US-0285142P.   |  |  |
| CC                    | CC and to produce other types of data and products dependent on DNA and      | PR 17-MAY-2001; 2001US-0291701P.   |  |  |
| CC                    | CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic   | PR 08-JUN-2001; 2001US-0296360P.   |  |  |
| CC                    | CC amino acid sequences of the invention. Note: The sequence data for this   | PR 10-JUL-2001; 2001US-030453P.  |  |  |
| CC                    | CC patent did not appear in the printed specification, but was obtained in   | PR 12-JUL-2001; 2001US-030455P.  |  |  |
| CC                    | CC electronic format directly from WIPO at                                   | PR 09-AUG-2001; 2001US-030486P.  |  |  |
| XX                    | CC ftp.wipo.int/pub/published_pct_sequences                                  | PR 13-AUG-2001; 2001US-031189P.  |  |  |
| XX                    | Sequence 843 AA;   | PR 16-AUG-2001; 2001US-0312337P.   |  |  |
| Query Match           | Score 418.5; DB 4;   | PR 18-OCT-2001; 2001US-031227P.  |  |  |
| Best Local Similarity | Length 843;  | PR 29-NOV-2001; 2001US-0334198P.   |  |  |
| Matches               | Pred. No. 3.1e-33;   |  |  |  |
| 78;                   | Conservative 30;   |  |  |  |
|                       | Mismatches 49;   |  |  |  |
|                       | Indels 1;  |  |  |  |
|                       | Gaps 1;  |  |  |  |
| PA                    | (CURA-) CURAGEN CORP.  |  |  |  |
| XX                    |  |  |  |  |
| OY                    | 11 ELPAAFPVQDDERWKAVLRLPCVSYLMVALGLITVIMSLILYORTLGGSKFCMCS 70                | PI Decristofaro MF, Pedigaru M, Miller C, Tchernev V, Zhong H;                 |  |  |
| Db                    | 665 ELPTATAQNDYGPQOKSSSSRPSCSLLVATAGLLTAVLISVLLQWLQGSNTCA 724                | PI Zhong M, Anderson D, Ballinger R, Gerlach V, Spytek KA, Rastelli L;         |  |  |
| OY                    | 71 QCSRCPNLUWMRNGSHCYFSMEKRDANSSLKFCADKGSHLILTEPDNQGVNLFQEYVGDF 130          | PI Kekuda R, Guo X, Zerhusen B, Andrew D, Mezes P, Patturajan M;               |  |  |
| Db                    | 725 SCPSPCRWPKYHCVSEKDNNSSLECLADSLLVITDNQEMSLLQVFLSEAF 784                   | PI Burgess CE, Eislen A, Wolenc A, Baumgartner J, Shinkets RA, Gusev V;        |  |  |
| OY                    | 131 YWIGLRIDLDGMEDGALSLSILSN-SVVKCGTIRH 167                                  | PI Verner CAM, Taupier RJ, Pena C, Shenoy S, Li L, Casman S, Boldog F;         |  |  |
| Db                    | 785 CWTGLRNNSGKWEDEGSPLNFSRNTCTIRKRHLHK 822                                  | PI Fernandes E, Smithson G, Malyankar U, Tailion B, Liu X;                     |  |  |
| XX                    |  | XX DR WPI; 2003-058504/05.   |  |  |
| XX                    |  | DR N-PSDB; ABT33363.   |  |  |
| XX                    |  | XX PT New polypeptides, designated as NOVX, useful for diagnosing and treating |  |  |
|                       |  | PT infections, neurological diseases, cancer, allergy, and bone,               |  |  |
|                       |  | PT immunological, skin, renal, brain, muscle and autoimmune disorders.         |  |  |
| XX                    |  | XX Claim 1; Page 118; 672pp; English.  |  |  |
| PS                    |  |  |  |  |

RESULT 10  
ABJ37898 standard; protein; 191 AA.  
ID ABJ37898

The invention relates to a novel isolated polypeptide, designated NOVX (NOV1 - 331), consisting of a mature form of one of 61 sequences, given in the specification, or its variant, where amino acid residue(s) in the variant differ from the mature form, provided that the variant differs in not more than 15 % of the amino acids from the sequence of the mature form. The NOVX polypeptides, nucleic acids encoding the polypeptides, and an antibody to the polypeptides, are useful for treating or preventing a NOVX-associated disorder in humans and for treating a syndrome associated with a human disease (NOVX-associated disorder). NOVX polypeptides and the encoding nucleic acids, are useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX polypeptide and polynucleotide, by measuring the level of polypeptide expression or the amount of nucleic acid from a mammal and comparing it with another mammal not having or not predisposed to the disease. NOVX polypeptide is also useful for identifying an agent that binds to NOVX and a cell expressing NOVX is useful for identifying an agent that modulates the expression or activity of NOVX. The ant bodies and a polypeptide having 95 % sequence identity to NOVX polypeptide are useful for treating a pathological state in a mammal. The antibodies are also useful for determining the presence or amount of NOVX in the sample. NOVX polypeptides, polynucleotides and antibodies specific for the polypeptides are useful for treating or preventing disorders or syndromes including trauma, viral, bacterial, fungal, protozoal, and parasitic infections. They can also treat disorders such as e.g., Alzheimer's disease or a stroke. The NOVX encoding nucleic acids are useful for expressing the NOVX proteins, to detect NOVX mRNA, or a genetic lesion in a NOVX gene and to modulate NOVX activity. NOVX sequences are also useful for identifying a cell or tissue type in a biological sample, to amplify DNA sequences from very small biological samples such as tissues e.g. hair or skin or body fluids in forensic biology and as primers and probes for use in identifying and/or cloning NOVX homologues in other cell types. The NOVX proteins are useful as an immunogen to generate antibodies which are useful for diagnostically monitoring protein levels and modulating NOVX activity. Cells comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. The NOVX nucleic acids can be used in gene therapy. This sequence represents a NOVX protein of the invention.

|     |  |
|-----|--|
| KW  | Mast cell function-associated antigen; MAFA; huMFA (E3/4-);  |
| KW  | splice variant; human; inflammation; allergy; asthma;  |
| KW  | rheumatoid arthritis; tumour; therapy.   |
| KX  |  |
| DS  | Homo sapiens .   |
| AX  | WO9854209-A2.  |
| PN  |  |
| XX  |  |
| XX  | 03-DEC-1998.   |
| PD  |  |
| XX  | 29-MAY-1998;   |
| PPF | 98WO-GB001572.   |
| PR  |  |
| XX  | 31-MAY-1997;   |
| PR  | 97GB-00011148.   |
| PA  |  |
| XX  | (PEPT-) PEPTIDE THERAPEUTICS LTD.  |
| PI  |  |
| PI  | Hewitt EL, Lamers MBAC, Lamont A, Williams DH;   |
| XX  |  |
| DR  | WPI; 1999-059806/05.   |
| DR  | N-PSDB; AAV84200.  |
| XX  |  |
| PPT | New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory diseases, and tumour growth. |
| PPT |  |
| PPT |  |
| XX  |  |

| Query  | Match   | Score              | DB         | Length     | 99; |
|--|---|--------------------|------------|------------|-----|
| Best Local Similarity  | 20.0*   | Score 207.5;       | DB 2;      | Length 99; |     |
| Matches 55;  | Best Local Similarity 29.6%;  | Prcd. No. 4.7e-13; |            |            |     |
| Matches 55;  | Conservative 12;  | Mismatches 30;     | Indels 89; | Gaps 1;    |     |
| Dy   | 1 MADNSIYSTLELPAAPIRQYDODSRWKVKAVILHRPCVSYLYMVALGLITVILMLIYQRTL     | 60                 |            |            |     |
| Dy   | 1 : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   | 61                 |            |            |     |
| Db   | 1 MTDSSVILSMILELTATQANQNDYGPQQKSSSSRSCLAVIAALGLLITAVILSVLIVQWLIL    | 60                 |            |            |     |
| Dy   | 61 CCCSKGFMQSQCSCRCRCPNLWMRNGSHCYYFSMERRDNWSSLKFCADKGSHLTFPDNQGVN   | 120                |            |            |     |
| Db   | 61 CQG-----   | 63                 |            |            |     |
| Dy   | 121 LFQEYVGDFYWIGLRIDGWRMEDGPALSLSILSNVYQKCGTIRRCGLHASSEVALQ        | 180                |            |            |     |
| Dy   | 121 : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : | 181                |            |            |     |
| Db   | 64 -----ISSNSFVQTCAITRKGHQASSCEVPLH                                 | 91                 |            |            |     |
| Dy   | 181 WICEKV 186  |                    |            |            |     |
| Db   | 181 : :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : | 97                 |            |            |     |
| RESULT 12  |   |                    |            |            |     |
| AAR54659   | ID AAR54659 standard; protein; 199 AA.                              |                    |            |            |     |
| XX   |   |                    |            |            |     |
| AC   | AAR54659;   |                    |            |            |     |
| XX   |   |                    |            |            |     |
| DT   | 25-MAR-2003 (revised)   |                    |            |            |     |
| DT   | 31-OCT-1994 (First entry)   |                    |            |            |     |
| XX   |   |                    |            |            |     |
| DE   | Human CD69.   |                    |            |            |     |
| XX   |   |                    |            |            |     |
| Immune system; thrombocyt development; signal transduction; probe. |   |                    |            |            |     |





QY 33 PCVSYLVWVALGLLTIVLMSLLYQRTLCGSSKGFMQSOSCRCPNLMMRNGSHCYFMSME 92  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 101 PC---MIVALAVIVL---QPSCSRPPF---SPVCPNAVGWFQGKCYFSDT 146  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 93 KRDWNSSLKFCADKGSHLLTFDNOGVNLFOYVGDFYWIGLDIDG--WRWEDGPAL 149  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 147 ESDWNSSREHCHRLGASLATLDTEEMEFMLQYQRPADRWGLHRAEGDEHWWTADSAF 206  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
QY 150 SLSLISNSVVO---KCGTIHRCGLIHASSEVALWICEK 185  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Db 207 T---NRPVFFELRGGRGCAYINGDGTSALCHSEKFWCSR 243  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: August 10, 2004, 16:16:29  
Job time : 47.5841 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:18:53 ; Search time 40.2619 Seconds  
 Perfect score: 1036  
 Sequence: 1 MADNSIYSTLELPAPRVQD.....GLHASSCEVALQWICKEKVLP 188

Scoring table: BLASTM62  
 GapP 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Database : Published Applications AA:  
 1: /cgm2\_6\_ptodata/2/pubpaas/us07\_pubcomb.pep:  
 2: /cgm2\_6\_ptodata/2/pubpaas/us07\_pubcomb.pep:  
 3: /cgm2\_6\_ptodata/2/pubpaas/us06\_pubcomb.pep:  
 4: /cgm2\_6\_ptodata/2/pubpaas/us06\_pubcomb.pep:  
 5: /cgm2\_6\_ptodata/2/pubpaas/us07\_new\_pub.pep:  
 6: /cgm2\_6\_ptodata/2/pubpaas/us09\_pubcomb.pep:  
 7: /cgm2\_6\_ptodata/2/pubpaas/us08\_pubcomb.pep:  
 8: /cgm2\_6\_ptodata/2/pubpaas/us08\_pubcomb.pep:  
 9: /cgm2\_6\_ptodata/2/pubpaas/us09\_pubcomb.pep:  
 10: /cgm2\_6\_ptodata/2/pubpaas/us09\_pubcomb.pep:  
 11: /cgm2\_6\_ptodata/2/pubpaas/us09\_pubcomb.pep:  
 12: /cgm2\_6\_ptodata/2/pubpaas/us09\_new\_pub.pep:  
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 16: /cgm2\_6\_ptodata/2/pubpaas/us10\_new\_pub.pep:  
 17: /cgm2\_6\_ptodata/2/pubpaas/us60\_pubcomb.pep:  
 18: /cgm2\_6\_ptodata/2/pubpaas/us60\_pubcomb.pep:  
 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

| Result No. | Score | Query | Match | Length | DB ID             | Description         |
|------------|-------|-------|-------|--------|-------------------|---------------------|
| 1          | 1036  | 100.0 | 188   | 9      | US-09-811-367B-5  | Sequence 5, Appli   |
| 2          | 838   | 80.9  | 188   | 9      | US-09-811-367B-3  | Sequence 3, Appli   |
| 3          | 545.5 | 52.7  | 189   | 14     | US-10-207-655-196 | Sequence 196, Appli |
| 4          | 525.5 | 50.7  | 189   | 9      | US-09-811-367B-1  | Sequence 1, Appli   |
| 5          | 184.5 | 17.8  | 199   | 10     | US-09-284-320-86  | Sequence 86, Appli  |
| 6          | 184.5 | 17.8  | 199   | 14     | US-10-207-655-182 | Sequence 182, Appli |
| 7          | 184.5 | 17.8  | 199   | 14     | US-10-179-528-3   | Sequence 3, Appli   |
| 8          | 184.5 | 17.8  | 199   | 15     | US-10-37-127-26   | Sequence 26, Appli  |
| 9          | 184   | 17.8  | 257   | 14     | US-10-179-528-4   | Sequence 4, Appli   |
| 10         | 182   | 17.6  | 268   | 15     | US-10-161-493-22  | Sequence 22, Appli  |
| 11         | 180   | 17.4  | 231   | 16     | US-10-451-843-1   | Sequence 1, Appli   |
| 12         | 179.5 | 17.3  | 265   | 9      | US-09-764-870-107 | Sequence 307, Appli |
| 13         | 179.5 | 17.3  | 265   | 14     | US-10-540-307     | Sequence 307, Appli |
| 14         | 179.5 | 17.3  | 275   | 15     | US-10-161-493-20  | Sequence 20, Appli  |
| 15         | 177.5 | 17.1  | 229   | 9      | US-09-989-722-424 | Sequence 424, Appli |

**ALIGNMENTS**

RESULT 1 US-09-811-367B-5

```

; Sequence 5, Application US/09811367B
; Patent No. US2003015510A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; ATTORNEY: Takahashi, Ng, Toshifumi
; APPLICANT: Miyakawa, Yoshiaki
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
; FILE REFERENCE: 021286/0278719
; CURRENT APPLICATION NUMBER: US/09-811,367B
; CURRENT FILING DATE: 2002/03/12
; PRIOR APPLICATION NUMBER: 601190,716
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 5
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus

```

US-09-811-367B-5

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Query Match 100.0%; Score 1036; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.7e-99;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MADNSIYSTLELPAPRYYODDSRWMKXAVLHRPCSYLVMVAGLTVILMSLLIQQTLL 60
 Db 1 MADNSIYSTLELPAPRYYODDSRWMKXAVLHRPCSYLVMVAGLTVILMSLLIQQTLL 60
 QY 61 CCGSKGMCSQCSPNLMWRNGSHCYFSMEKRDNSSLKEADGSHLLTFPDNGSVN 120
 Db 61 CCGSKGMCSQCSPNLMWRNGSHCYFSMEKRDNSSLKEADGSHLLTFPDNGSVN 120
 QY 121 LFQBYGEDDFYWGFLRIDLIDGMRWEDGPALSLSLTSLSNSVVKCGTIIHRCGLHASCEYALQ 180
 Db 121 LFQBYGEDDFYWGFLRIDLIDGMRWEDGPALSLSLTSLSNSVVKCGTIIHRCGLHASCEYALQ 180

QY 181 WICEKVL 188  
Db 181 WICEKVL 188

**RESULT 2**  
US-09-811-367B-3  
Sequence 3, Application US/09811367B  
Patent No. US20020155110A1  
GENERAL INFORMATION:  
APPLICANT: GEMINI SCIENCE, INC.  
APPLICANT: Takahashi, No. US20020155110Auaki  
APPLICANT: Mikayama, Toshiyumi  
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MATA)  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM  
FILE REFERENCE: 021286/0278719  
CURRENT APPLICATION NUMBER: US/09/811-367B  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/190,716  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 20  
SEQ ID NO 3  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-811-367B-3

Query Match 80.9%; Score 838; DB 9; Length 188;  
Best Local Similarity 80.7%; Pred. No. 9.7e-79;  
Matches 151; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MADNSIYSTLEPAPVQDSSRWKAVLHRPCVSILVMAGLITVILSLLYORTL 60  
Db 1 MADSSIYSTLEPAPQYQDESRWKAVLHRPHLSRFAVMGLITVILSLLYQRIL 60

QY 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVN 120  
Db 61 CCSSKDSCTCSHBCSPCLLWTRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVK 120

QY 121 LFOBYVGEDFYWIGLRIDGWRMEDGPALSLSILSNSYVKCOTIHRCGLHASSCEVALQ 180  
Db 121 LFGSYLGDDFYWIGLRNLDGWRMEGGPAISRLTINSLIQRCAIHNGLQASSCEVALQ 180

QY 181 WICEKVL 187  
Db 181 WICKVL 187

**RESULT 3**  
US-10-207-655-196  
Sequence 196, Application US/10207655  
Publication No. US20030118592A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Ledbetter, Jeffrey A.  
TITLE OF INVENTION: BINDING DOMAIN IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 3900540C1  
CURRENT APPLICATION NUMBER: US/10/207,655  
CURRENT FILING DATE: 2002-07-25  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 196  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-207-655-196

Query Match 52.7%; Score 545.5; DB 14; Length 189;  
Best Local Similarity 55.1%; Pred. No. 2.3e-48;  
Matches 103; Conservative 28; Mismatches 55; Indels 1; Gaps 1;

QY 1 MADNSIYSTLEPAPVQDSSRWKAVLHRPCVSILVMAGLITVILSLLYORTL 60  
Db 1 MTDSSVYSMLPEFTQADQNDYGPQKSSSSRPSCSCLVATLGLITAVLSSLYQWL 60

QY 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVN 120  
Db 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVK 120

QY 121 LFOBYVGEDFYWIGLRIDGWRMEDGPALSLSILSNSYVKCOTIHRCGLHASSCEVALQ 179  
Db 121 LLQVFLSEAFCNGLRNNSGRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180

QY 180 QWICKEKV 186  
Db 181 HGCKKV 187

**RESULT 4**  
US-09-811-367B-1  
Sequence 1, Application US/09811367B  
Patent No. US20020155110A1  
GENERAL INFORMATION:  
APPLICANT: GEMINI SCIENCE, INC.  
APPLICANT: Takahashi, No. US20020155110Auaki  
APPLICANT: Mikayama, Toshiyumi  
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MATA)  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM  
FILE REFERENCE: 021286/0278719  
CURRENT APPLICATION NUMBER: US/09/811-367B  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/190,716  
PRIOR FILING DATE: 2000-03-17  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-811-367B-1

Query Match 50.7%; Score 525.5; DB 9; Length 189;  
Best Local Similarity 53.5%; Pred. No. 2.7e-16;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

QY 1 MADNSIYSTLEPAPVQDSSRWKAVLHRPCVSILVMAGLITVILSLLYORTL 60  
Db 1 MTDSSVYSMLPEFTQADQNDYGPQKSSSSRPSCSCLVATLGLITAVLSSLYQWL 60

QY 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVN 120  
Db 61 CCGSKGFMCSQCSRCPNLWMRNGSHCYFSMERRDNSSLKEADKSHLLTFPDNGGVK 120

QY 121 LFOBYVGEDFYWIGLRIDGWRMEDGPALSLSILSNSYVKCOTIHRCGLHASSCEVALQ 179  
Db 121 LLQVFLSEAFCNGLRNNSGRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180

QY 180 QWICKEKV 186  
Db 181 HGCKKV 187

**RESULT 5**  
US-09-284-320-86  
Sequence 86, Application US/09284320  
Publication No. US20030022175A1  
GENERAL INFORMATION:  
APPLICANT: Kato, Seishi et al.  
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs  
FILE REFERENCE: GIN-6705CPUS  
CURRENT APPLICATION NUMBER: US/09/284,320  
CURRENT FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: JP 8-301429

PRIOR FILING DATE: 1996-11-13  
 PRIOR APPLICATION NUMBER: PCT/JP97/040556  
 PRIOR FILING DATE: 1997-11-07  
 NUMBER OF SEQ ID NOS: 91  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 86  
 LENGTH: 199  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US -09-284-320-86

Query Match 17.8%; Score 184.5; DB 10; Length 199;  
 Best Local Similarity 26.3%; Pred. No. 7.2e-11;  
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSILVMVALGLTVILMSSLLYQRTLCCGSKGFMC--SQCSCRCPNLWNRNGSHCYYFNM 91  
 Db 45 VMNVYFVITLIALTSQYN--CPGQYTFSMPSDSHVSSCSEDWYGQYQRCKYPIST 101  
 Qy 92 EKRDWNSSLKFADKGSHLTLFPDNQGVNLFQEYVGDFFYWIQLRDIQ--WWEDEGPAL 149  
 Db 102 VKRSHTSQAQCSEGATLAVIDSEKDMMFLKRYAGREEHWVLKKEPPHPWKNSNGKEF 161  
 Qy 150 SLSLISNSVYQKCGFTHRCGHHASCEVAIQLWICK 185  
 Db 162 N-NWFNTVGSDDKCVFLKNTEVSSMECKNLYWICKN 196

RESULT 6  
 US-10-207-655-182  
 Sequence 182, Application US/10207655  
 GENERAL INFORMATION:  
 APPLICANT: Ledbetter, Jeffrey A.  
 APPLICANT: Hayden-Jedbetter, Martha S.  
 TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
 FILE REFERENCE: 390069.401C1  
 CURRENT APPLICATION NUMBER: US/10/207,655  
 CURRENT FILING DATE: 2002-07-25  
 NUMBER OF SEQ ID NOS: 426  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 182  
 LENGTH: 199  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-207-655-182

Query Match 17.8%; Score 184.5; DB 14; Length 199;  
 Best Local Similarity 26.3%; Pred. No. 7.2e-11;  
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

QY 35 VSILVMVALGLTVILMSSLLYQRTLCCGSKGFMC--SQCSCRCPNLWNRNGSHCYYFNM 91  
 Db 45 VMNVYFVITLIALTSQYN--CPGQYTFSMPSDSHVSSCSEDWYGQYQRCKYPIST 101  
 Qy 92 EKRDWNSSLKFADKGSHLTLFPDNQGVNLFQEYVGDFFYWIQLRDIQ--WWEDEGPAL 149  
 Db 102 VKRSHTSQAQCSEGATLAVIDSEKDMMFLKRYAGREEHWVLKKEPPHPWKNSNGKEF 161  
 Qy 150 SLSLISNSVYQKCGFTHRCGHHASCEVAIQLWICK 185  
 Db 162 N-NWFNTVGSDDKCVFLKNTEVSSMECKNLYWICKN 196

RESULT 8  
 US-10-207-655-182  
 Sequence 182, Application US/10207655  
 GENERAL INFORMATION:  
 APPLICANT: Entage, Peter C.R.  
 APPLICANT: Dernach, Radje  
 APPLICANT: Goodrich, Ryle  
 APPLICANT: Tang, Y. Tom  
 TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TAR  
 FILE REFERENCE: NUVO-01CIP  
 CURRENT APPLICATION NUMBER: US/10/379,127  
 CURRENT FILING DATE: 2003-03-03  
 PRIOR APPLICATION NUMBER: US 09/799,451  
 PRIOR FILING DATE: 2001-03-05  
 NUMBER OF SEQ ID NOS: 27

RESULT 7  
 US-10-179-528-3  
 Sequence 3, Application US/10179528  
 GENERAL INFORMATION:  
 APPLICANT: Badman, Olga  
 APPLICANT: Shah, Purvi  
 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
 NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/179,528  
 FILING DATE: 24-Jun-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/846,523  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0281 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-845-0555  
 TELEX: 415-845-4166  
 TELE: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 291898  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-10-179-528-3

Query Match 17.8%; Score 184.5; DB 14; Length 199;  
 Best Local Similarity 26.3%; Pred. No. 7.2e-11;  
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

Qy 35 VSILVMVALGLTVILMSSLLYQRTLCCGSKGFMC--SQCSCRCPNLWNRNGSHCYYFNM 91  
 Db 45 VMNVYFVITLIALTSQYN--CPGQYTFSMPSDSHVSSCSEDWYGQYQRCKYPIST 101  
 Qy 92 EKRDWNSSLKFADKGSHLTLFPDNQGVNLFQEYVGDFFYWIQLRDIQ--WWEDEGPAL 149  
 Db 102 VKRSHTSQAQCSEGATLAVIDSEKDMMFLKRYAGREEHWVLKKEPPHPWKNSNGKEF 161  
 Qy 150 SLSLISNSVYQKCGFTHRCGHHASCEVAIQLWICK 185  
 Db 162 N-NWFNTVGSDDKCVFLKNTEVSSMECKNLYWICKN 196

SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 26  
 LENGTH: 199  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-379-127-26

Query Match 35 VSYLVWVAGLGLTVILMSSLXORTIICGSKGFM--SQCSRCPNLUWRNGSHCYXFSM 91  
 Best Local Similarity 26.3%; Pred. No. 7.2e-11;  
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

Qy 45 VMNVVFPTILIALIAASVGQN--CPGQYTFMSPSDHSVSSCSEIWVGYQRKCYFIST 101  
 Db 92 EKRDWNSSLKFCADKGSHLIPPDNQCVNLFOEYGVDFYWIQLRDLDG--WRWEIGPAL 149  
 Db 102 VKRSTWISAQNACSEHGBTLAVIDSEKMMNFKRYAAGRHEHWYGLKEUPGHWPKWSNGKEF 161  
 Qy 150 SLSLILSNVVQKCGTHTRCGLHASSEVALQWICEK 185  
 Db 162 N-NWFNTVGSDKCVFLRNTEVSSMECKNLWICNK 196

---

RESULT 9 US-10-179-528-4  
 Sequence 4, Application US/10179528  
 Publication No. US201030166132A1  
 GENERAL INFORMATION:  
 APPLICANT: Bandman, Olga  
 Shah, Purvi  
 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 93304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Discrete  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/179,528  
 FILING DATE: 24-Jun-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/846,523  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,7449  
 REFERENCE/DOCKET NUMBER: PF-0281 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEX: 415-945-4166  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 257 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 505325  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 17.8% Score 184; DB 14; Length 257;

Best Local Similarity 28.6%; Pred. No. 1.1e-10;  
 Matches 46; Conservative 23; Mismatches 66; Indels 26; Gaps 6;

Qy 33 PCVSYLWVAGLGLTVILMSSLXORTIICGSKGFMCSQCSRCPNLUWRNGSHCYXFSM 92  
 Db 101 PC----MLVLAVALVYV----QRPSCSPRPPF---SHVCPNAWVGFQCKCYFSDT 146

Qy 93 KRDWNSSLKFCADKGSHLIPPDNQCVNLFOEYGVDFYWIQLRDLDG--WRWEIGPAL 149  
 Db 147 ESDWNSREHCHRGLSLATLDKEEMEFMLQYQEPADRNLGHRAEGDEHWTWADGSAF 206

Qy 150 SLSLILSNVVQKCGTHTRCGLHASSEVALQWICEK 185  
 Db 207 T---NRPVFLERGGRCAYINGDGISSALCHSEKFVWCSR 243

RESULT 10 US-10-161-493-22  
 Sequence 22, Application US/10161493  
 Publication No. US2004001855A1  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, David W  
 Zerhusen, Bryan D  
 APPLICANT: Li, Li  
 APPLICANT: Zhong, Mei  
 APPLICANT: Casman, Stacie J  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Shimkets, Richard A  
 APPLICANT: Gorman, Linda  
 APPLICANT: Pena, Carol EA  
 APPLICANT: Kekuda, Ramesh  
 APPLICANT: Paturajan, Meera  
 APPLICANT: Spytek, Kimberly A  
 APPLICANT: Leite, Mario W  
 APPLICANT: Rastelli, Luca  
 APPLICANT: MacDougall, John R  
 APPLICANT: Taupier Jr., Raymond J  
 APPLICANT: Guo, Xiaojia Sasha  
 APPLICANT: Miller, Charles E  
 APPLICANT: Shenoy, Suresh G  
 APPLICANT: Hjalt, Tord  
 APPLICANT: Voss, Edward Z  
 APPLICANT: Boldog, Ferenc L  
 APPLICANT: Malayankar, Uriel M  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Ji, Weizhen  
 APPLICANT: Smithson, Glenna  
 APPLICANT: Edinger, Shlomit R  
 APPLICANT: Millet, Isabelle  
 APPLICANT: Ellerman, Karen  
 TITLE OF INVENTION: No. US2004001855A1el Antibodies that Bind to Antigenic Polypeptides  
 FILE REFERENCE: Acids Encoding the Antigens, and Methods of Use  
 CURRENT APPLICATION NUMBER: US/10/161,493  
 CURRENT FILING DATE: 2002-06-03  
 PRIOR APPLICATION NUMBER: 60/295,607  
 PRIOR FILING DATE: 2001-06-04  
 PRIOR APPLICATION NUMBER: 60/337,524  
 PRIOR FILING DATE: 2001-11-16  
 PRIOR APPLICATION NUMBER: 60/296,404  
 PRIOR FILING DATE: 2001-06-06  
 PRIOR APPLICATION NUMBER: 60/296,418  
 PRIOR FILING DATE: 2001-06-05  
 PRIOR APPLICATION NUMBER: 60/296,575  
 PRIOR FILING DATE: 2001-06-07  
 PRIOR APPLICATION NUMBER: 60/359,151  
 PRIOR FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 60/297,414  
 PRIOR FILING DATE: 2001-06-11  
 PRIOR APPLICATION NUMBER: 60/297,573  
 PRIOR FILING DATE: 2001-06-12  
 PRIOR APPLICATION NUMBER: 60/341,143  
 PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/297,567  
*i* Remaining Prior Application data removed - See file Wrapper or PALM.  
*i* NUMBER OF SEQ ID NOS: 299  
*i* SEQ ID NO: 22  
*i* LENGTH: 268  
*i* TYPE: PRT  
*i* ORGANISM: Homo sapiens  
 US-10-161-493-22

Query Match 17.6%; Score 182; DB 15; Length 268;  
 Best Local Similarity 31.5%; Pred. No. 1.9e-10; Indels 12; Gaps 5;  
 Matches 40; Conservative 22; Mismatches 53; Gaps 5;

Qy 71 QCSRCPNLWMEENGSHCYXFSM-EKRNWNSSKECADKGSHLITFP--DNGQVNLFOEYVG 127  
 Db 131 RCNPCKPKMOWQVNQNSCYFTNEEKWANSERKDIDNNTSLVKIDSLEERDFLMQSPLLM 190

Qy 128 EDFYWIGLR-DIDG--WRWEDGPALSLLSNSTVQK----CGTIIHRCGLHASCEVA 178  
 Db 191 FSEFWIGLSQDSSGRWFWEGSVRPSPSLEFTKEKDQINGSKGGCAYFQRNITYISRCDAE 250

Qy 179 LQWICBK 185  
 Db 251 IFWICEK 257

RESULT 11  
 US-10-451-843-1  
*i* sequence 1, Application US/10451843  
*i* Publication No. US20040115738A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: INNATE PHARMA S.A.S.  
*i* TITLE OF INVENTION: Peptides having a triggering NK receptor activity and biology  
*i* TITLE OF INVENTION: Polypeptides having a triggering NK receptor activity and biology  
*i* FILE REFERENCE: 1243NKP80  
*i* CURRENT APPLICATION NUMBER: US/10/451,843  
*i* CURRENT FILING DATE: 2003-12-30  
*i* NUMBER OF SEQ ID NOS: 2  
*i* SEQ ID NO: 1  
*i* LENGTH: 231  
*i* TYPE: PRT  
*i* ORGANISM: Homo sapiens  
 US-10-451-843-1

Query Match 17.4%; Score 180; DB 16; Length 231;  
 Best Local Similarity 21.8%; Pred. No. 2.5e-10; Indels 82; Gaps 11;  
 Matches 54; Conservative 38; Mismatches 74; Gaps 11;

Qy 1 MADNSIYSTL-PAPRQVQDDSRMKVAKLHRPCVS-----YLWVAL----GL 45  
 Db 1 MQDEERYMLNVSQ-----KKRSAQTSCLTFKDYSVTLLHWYCLLGSFTYNG 50

Qy 46 LTVIIMSLIYQRTLCCG-----SKGFMCQSQCSR-----74  
 Db 51 LTLLTLLSLI-----LVSCGYLTKCQKG-SSSNATQYEDTDLKYNGTERNNISKDLCSR 106

Qy 75 -----CPLWMRNGSHCYYSFMSKRDWNSLRFCDKGSHLITFPDNGVNLFOEYVG 127  
 Db 107 SADQTVLQSEWILKYQGKCYWFSENEMKMSDSTVYCLEFKSHLLIHDQLEMFIQKRLN 166

Qy 128 E-DYWIGLRDID--GWWEVDGPALSLL-----SNSVYQKCGPTIHRCGIHASSC 176  
 Db 167 QLNWVWGNINFSLRMTWWDGSPIDSKIFFKPAKENS---CAAIKESKIFSETCS 222

Qy 177 VALOWICE 184  
 Db 223 SVFRWICQ 230

RESULT 12

US-09-764-870-307  
*i* Sequence 307, Application US/09764870  
*i* Patent No. US20042386A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: Rosen et al.  
*i* TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
*i* FILE REFERENCE: PTZ14  
*i* CURRENT APPLICATION NUMBER: US/09/764,870  
*i* CURRENT FILING DATE: 2003-01-17  
*i* Prior application data removed - consult PALM or file wrapper  
*i* NUMBER OF SEQ ID NOS: 646  
*i* SOFTWARE: PatentIn Ver. 2.0  
*i* SEQ ID NO: 307  
*i* LENGTH: 265  

Query Match 17.3%; Score 179.5; DB 9; Length 265;  
 Best Local Similarity 26.4%; Pred. No. 3.4e-10; Indels 65; Gaps 11;  
 Matches 64; Conservative 29; Mismatches 84;

Qy 1 MADNSIYSTL--ELPAAAPRQVQDDSRMKVAKLHRPC--VSYLVNM----ALGLITVILM 51  
 Db 25 MHEEEIYTSLQWDSAPDTYQ-----KCLSSNRKSGACCLVMVISCVFCMGLLTASIF 77

Qy 52 -----SLLIYQRTL-----CCGSKGMCS-----QCSR 75  
 Db 78 LGVKLQLQVSTIAMQQEKLQIQQERALLNFTWRSCLAMKYCQAFMONSLSSAHNSPPC 137

Qy 76 PNLMWRNGSHCYYSFMSKRDWNSLRFCDKGSHLITFPDNOGYNL----FOEYVGEDFY 131  
 Db 138 PNNWQNTRSCYYSEIWSIWHTSQENLREGSTLQIESKEENDFTSSLRKIGSYND 197

Qy 132 WIGLRDIDG----NRWEDGPALSLSI----SNSVYQKCGPTIHRCGIHASSC 183  
 Db 198 WVGLSQ-DGHSGRWIWDQDSSPSPGQLPAAERSQANOVCGVYKNSLSSNCSTWKFYFIC 256

Qy 184 EK 185  
 Db 257 EK 258

RESULT 13  
 US-10-125-540-307  
*i* Sequence 307, Application US/10125540  
*i* Publication No. US20030059875A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: Rosen et al.  
*i* TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
*i* FILE REFERENCE: PTZ14C1  
*i* CURRENT APPLICATION NUMBER: US/10/125,540  
*i* CURRENT FILING DATE: 2002-04-19  
*i* Prior application removed - See File Wrapper or Palm  
*i* NUMBER OF SEQ ID NOS: 646  
*i* SOFTWARE: PatentIn Ver. 2.0  
*i* SEQ ID NO: 307  
*i* LENGTH: 265  

Query Match 17.3%; Score 179.5; DB 14; Length 265;  
 Best Local Similarity 26.4%; Pred. No. 3.4e-10; Indels 65; Gaps 11;  
 Matches 64; Conservative 29; Mismatches 84;

Qy 1 MADNSIYSTL--ELPAAAPRQVQDDSRMKVAKLHRPC--VSYLVNM----ALGLITVILM 51  
 Db 25 MHEEEIYTSLQWDSAPDTYQ-----KCLSSNRKSGACCLVMVISCVFCMGLLTASIF 77

Qy 52 -----SLLIYQRTL-----CCGSKGMCS-----QCSR 75  
 Db 78 LGVKLQLQVSTIAMQQEKLQIQQERALLNFTWRSCLAMKYCQAFMONSLSSAHNSPPC 137

76 PNLWMRNGSHCYYSMEKRDWNSSLKCADKGSHLTFPDNQGYNL---FQEYVGDFY 131  
 SEQ :|||:|||:|||:|||:|||:|||:  
 Db 138 PNNWLNQRESCYYVSEWISWIHTWSOQNCLKEGSTLUQIEEREMDFTGSLRKTKGSYDY 197  
 ; SEQ ID NO: 20  
 ; LENGTH: 275  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-161-493-20

RESULT 14  
 US-10-161-493-20  
 ; Sequence 20, Application US/10161493  
 ; Publication No. US20040018555A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, David W  
 ; APPLICANT: Zerhusen, Bryan D  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Zhong, Mei  
 ; APPLICANT: Casman, Stacie J  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Shimkets, Richard A  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Pena, Carol EA  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Spytek, Kimberly A  
 ; APPLICANT: Leite, Mario W  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: MacDougall, John R  
 ; APPLICANT: Taupier Jr., Raymond J  
 ; APPLICANT: Guo, Xiaoqia Sacha  
 ; APPLICANT: Miller, Charles E  
 ; APPLICANT: Shenoy, Suresh G  
 ; APPLICANT: Hjalt, Tord  
 ; APPLICANT: Voss, Edward Z  
 ; APPLICANT: Boldog, Ferenc L  
 ; APPLICANT: Malyankar, Uriel M  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Ji, Weizhen  
 ; APPLICANT: Smithson, Glenna  
 ; APPLICANT: Edinger, Shlomit R  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Ellerman, Karen  
 ; TITLE OF INVENTION: No. US20040018555A1 Antibodies that Bind to Antigenic Polypeptides  
 ; TITLE OF INVENTION: Methods of Use  
 ; FILE REFERENCE: 21402-377A  
 ; CURRENT APPLICATION NUMBER: US/10/161-493  
 ; CURRENT FILING DATE: 2002-06-03  
 ; PRIOR APPLICATION NUMBER: 60/295, 607  
 ; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: 60/337, 524  
 ; PRIOR FILING DATE: 2001-11-16  
 ; PRIOR APPLICATION NUMBER: 60/296, 404  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: 60/296, 418  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: 60/296, 575  
 ; PRIOR FILING DATE: 2001-06-07  
 ; PRIOR APPLICATION NUMBER: 60/359, 151  
 ; PRIOR FILING DATE: 2002-02-21  
 ; PRIOR APPLICATION NUMBER: 60/297, 414  
 ; PRIOR FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: 60/297, 573  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: 60/341, 143  
 ; PRIOR FILING DATE: 2001-12-14  
 ; PRIOR APPLICATION NUMBER: 60/297, 567  
 ; PRIOR FILING DATE: 2001-06-12

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 299  
; SEQ ID NO: 20  
; LENGTH: 275  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-161-493-20

Query Match 17.3%: Score 179.5; DB 15; Length 275;  
Best Local Similarity 31.5%; Pred. No. 3.5e-10; Mismatches 56; Indels 11; Gaps 5;

Matches 41; Conservative 2;

Qy 67 FMCSQCSRCPNLMWNRNGSHCYYSM-EKRDNNSLKF CADKGSHLTFP-DNQGYNLFQ 123  
Db 135 FSDHRCNPCCPQWQYQNSCYFTNEEKWTANSRDCIDNSTVKIDSLEEDFLMSQ 194

Qy 124 BYVGEDFYWIGLR-DIDG--WRWEDGPALSLSILNSVVQ---KCGTIIHRKGHLASSC 175  
Db 195 PLIMFSEFWNLGLSWSSGRSMNEWEDGSVPSPSLSITKELDQINGSKSCAYFQKNTYISRC 254

Qy 176 EVALQWCEK 185  
Db 255 SAEIWICEK 264

RESULT 15  
US-09-989-722-424  
; Sequence 424, Application US/09989722  
; Patent No. US20072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers Luc C  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kliavkin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumans, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; ACIDS Encoding the Same  
; FILE REFERENCE: P2130P1c63  
; CURRENT APPLICATION NUMBER: US/09/989-722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/06516  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088036
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088332
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088433
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02

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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match Score 177.5; DB 9; Length 229;
Best Local Similarity 26.9%; Pred. No. 4.5e-10;
Matches 61; Conservative 32; Mismatches 83; Indels 51; Gaps 12;

Qy 1 MADNSTYSTLED----PAAPRV-QDPSRWKVA-VLHRPCVSYLV-MVALGLLTIVLMS 52
Db 1 MODEDGITLNKTRKALVSVGPASSWWRMALLILCIVGMVVGLVAIGIWSMQRN 60
Qy 53 LLLYORTLCCGS-----KG-FMCSQCSRCPNLWNRNGSHCYYSFMEK 93
Db 61 YIQDENENRTGTIQLAKRFQCVVVKQSELKGTFKGHKCSPCDTMRYYGDSCYGFRRHN 120

Qy 94 RDWNSSLKPCADKGSHLITPDNQGVNLFOEYVGEDTY--WIGL--RDIDGWRREDGP 147
Db 121 LTWEESROYCTDMNATLKKI-DNRNI---VEVTKARTHLLIRVGLSRQKSNEWVKHEDG- 175

Qy 148 ALSLSILSNSVVO-----KCGTIIHRCGLHASSEVALOWICEK 185
Db 176 ---SVISENMFFLEDGKGNMNCAYFHNGKHEPTECNKHYLMCER 218

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Search completed: August 10, 2004, 16:32:38  
 Job time : 41.2619 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:13:57 ; Search time 14.6407 Seconds  
 (without alignments)  
 662.924 million cell updates/sec

Title: US-09-811-367B-5

Perfect score: 1036

Sequence: 1 MADNSIYSTLEDPAAPRQD.....GHASSCEVALQWICHEKVLP 188

Scoring table: BILOSUM62

Gappen: 10.0 , Gapext: 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 100%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgn2\_6/.ptodata/2/iaa/5A\_COMB\_pep:  
 2: /cgn2\_6/.ptodata/2/iaa/5B\_COMB\_pep:  
 3: /cgn2\_6/.ptodata/2/iaa/6A\_COMB\_pep:  
 4: /cgn2\_6/.ptodata/2/iaa/6B\_COMB\_pep:  
 5: /cgn2\_6/.ptodata/2/iaa/pctus\_COMB\_pep:  
 6: /cgn2\_6/.ptodata/2/iaa/backfiles\_pep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID             | Description        | Score | Query | Match | Length | DB ID            | Description       |
|------------|-------|-------|-------|--------|-------------------|--------------------|-------|-------|-------|--------|------------------|-------------------|
| 1          | 1036  | 100.0 | 188   | 3      | US-09-722-126A-5  | Sequence 5, Appli  | 166   | 100.0 | 188   | 3      | US-09-722-126A-8 | Sequence 5, Appli |
| 2          | 1036  | 100.0 | 188   | 5      | PCT-US95-04258-5  | Sequence 5, Appli  | 166   | 5     | 115   | 5      | PCT-US95-04258-5 | Sequence 5, Appli |
| 3          | 651   | 62.8  | 114   | 3      | US-09-722-126A-6  | Sequence 6, Appli  | 166   | 5     | 114   | 3      | US-09-722-126A-6 | Sequence 6, Appli |
| 4          | 651   | 62.8  | 114   | 5      | PCT-US95-04258-6  | Sequence 6, Appli  | 166   | 5     | 114   | 5      | PCT-US95-04258-6 | Sequence 6, Appli |
| 5          | 273   | 26.4  | 76    | 4      | US-09-531-056A-23 | Sequence 23, Appli | 184   | 5     | 17.8  | 5      | PCT-US93-0418-2  | Sequence 2, Appli |
| 6          | 184   | 5     | 17.8  | 199    | 5                 | PCT-US93-0418-2    | 175   | 5     | 16.9  | 199    | 3                | US-08-772-440-13  |
| 7          | 175   | 5     | 16.9  | 229    | 4                 | US-08-772-440-13   | 174   | 5     | 16.8  | 191    | 4                | US-09-531-056A-6  |
| 8          | 175   | 5     | 16.9  | 229    | 4                 | US-09-247-155-97   | 169   | 5     | 16.4  | 225    | 2                | US-08-738-462-2   |
| 9          | 174   | 5     | 16.8  | 191    | 4                 | US-09-531-056A-6   | 164   | 5     | 16.4  | 225    | 2                | US-08-738-462-2   |
| 10         | 169   | 5     | 16.4  | 225    | 2                 | US-08-738-462-2    | 164   | 5     | 16.4  | 225    | 2                | US-08-738-462-2   |
| 11         | 169   | 5     | 16.4  | 225    | 5                 | PCT-US94-07587-2   | 164   | 5     | 16.1  | 115    | 3                | US-09-111-470-4   |
| 12         | 166   | 5     | 16.1  | 115    | 3                 | US-09-111-470-4    | 166   | 5     | 16.1  | 115    | 5                | PCT-US95-04258-5  |
| 13         | 166   | 5     | 16.1  | 115    | 5                 | PCT-US95-04258-5   | 166   | 5     | 16.1  | 190    | 4                | US-09-111-470-4   |
| 14         | 166   | 5     | 16.1  | 190    | 3                 | US-09-111-470-4    | 164   | 5     | 15.9  | 273    | 3                | US-09-111-470-10  |
| 15         | 164   | 5     | 15.9  | 191    | 4                 | US-09-111-470-10   | 164   | 5     | 15.9  | 292    | 2                | US-08-688-342-4   |
| 16         | 164   | 5     | 15.9  | 292    | 2                 | US-08-688-342-4    | 164   | 5     | 15.9  | 292    | 2                | US-08-688-342-4   |
| 17         | 164   | 5     | 15.9  | 292    | 2                 | US-08-688-342-4    | 164   | 5     | 15.9  | 292    | 2                | US-08-688-342-4   |
| 18         | 164   | 5     | 15.9  | 316    | 3                 | US-09-111-470-4    | 164   | 5     | 15.9  | 316    | 3                | US-09-111-470-4   |
| 19         | 161   | 5     | 15.6  | 194    | 4                 | US-09-111-470-4    | 161   | 5     | 15.6  | 190    | 4                | US-09-111-470-4   |
| 20         | 161   | 5     | 15.6  | 201    | 2                 | US-09-111-470-4    | 161   | 5     | 15.6  | 201    | 2                | US-09-111-470-4   |
| 21         | 161   | 5     | 15.6  | 201    | 2                 | US-09-111-470-4    | 158   | 5     | 15.3  | 167    | 2                | US-08-772-440-21  |
| 22         | 158   | 5     | 15.3  | 209    | 3                 | US-08-772-440-21   | 158   | 5     | 15.3  | 209    | 3                | US-08-772-440-21  |
| 23         | 158   | 5     | 15.3  | 1487   | 3                 | US-08-840-062-7    | 158   | 5     | 15.3  | 1487   | 3                | US-08-840-062-7   |
| 24         | 157   | 5     | 15.2  | 216    | 3                 | US-08-246B-9       | 157   | 5     | 15.2  | 216    | 3                | US-08-246B-9      |
| 25         | 157   | 5     | 15.2  | 216    | 3                 | US-08-543-246B-24  | 157   | 5     | 15.2  | 328    | 4                | US-09-531-056A-13 |
| 26         | 157   | 5     | 15.2  | 216    | 3                 | US-08-543-246B-24  | 157   | 5     | 15.2  | 328    | 4                | US-08-543-246B-24 |
| 27         | 157   | 5     | 15.2  | 237    | 3                 | US-09-111-470-2    | 157   | 5     | 15.2  | 237    | 3                | US-09-111-470-2   |

#### ALIGNMENTS

RESULT 1  
 US-09-722-126A-5  
 Sequence 5, Application US/08722126A  
 Patent No. 6034227

GENERAL INFORMATION:  
 APPLICANT: PECHT, Israel  
 APPLICANT: GOTTEMANN, Marcelo D.  
 APPLICANT: TAL, Michael  
 TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/722,126A  
 FILING DATE: 08-OCT-1996  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04258  
 FILING DATE: 06-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 109257  
 FILING DATE: 08-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25, 618  
 REFERENCE/DOCKET NUMBER: PECHT=1A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTISTICS:  
 LENGTH: 188 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-722-126A-5  
 Query Match 100.0%; Score 1036; DB 3; Pred. No. 1.3e-105;  
 Best Local Similarity 100.0%; Score 1036; DB 3; Pred. No. 1.3e-105;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MADNSIYSTLELPAPVQDDSRWKAVLHRPCVSILYVVALGLTIVMLSLILYQRTL 60 Db 1 MADNSIYSTLELPAPVQDDSRWKAVLHRPCVSILYVVALGLTIVMLSLILYQRTL 60 Qy 1 CGGSKGMCSQCSRCPNLWNRNGSHCYFSMEKRDWNSLKFCAKGSHLLTFPDNQGVN 120 Db 1 CGGSKGMCSQCSRCPNLWNRNGSHCYFSMEKRDWNSLKFCAKGSHLLTFPDNQGVN 120 RESULT 3 US-08-722-126A-6 Sequence 6, Application US/08722126A Patent No. 6034227 GENERAL INFORMATION: APPLICANT: PECHT, Israel APPLICANT: GUTHMANN, Marcelo D. APPLICANT: TAL, Michael TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN (MAFA) NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C. COUNTRY: UNITED STATES OF AMERICA ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/722-126A FILING DATE: 08-OCT-1996 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04258 FILING DATE: 06-APR-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: IL 109257 FILING DATE: 06-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618 REFERENCE/DOCKET NUMBER: PECHT=1A TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 658-5197 TELEFAX: (202) 737-3528 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 114 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-722-126A-6 Query Match 62.8%; Score 651; DB 3; Length 114; Best Local Similarity 100.0%; Pred. No. 9.7e-64; Mismatches 0; Indels 0; Gaps 0; Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 MADNSIYSTLELPAPVQDDSRWKAVLHRPCVSILYVVALGLTIVMLSLILYQRTL 60 Db 1 MADNSIYSTLELPAPVQDDSRWKAVLHRPCVSILYVVALGLTIVMLSLILYQRTL 60 Qy 1 CGGSKGMCSQCSRCPNLWNRNGSHCYFSMEKRDWNSLKFCAKGSHLLTFPDNQGVN 120 Db 1 CGGSKGMCSQCSRCPNLWNRNGSHCYFSMEKRDWNSLKFCAKGSHLLTFPDNQGVN 120 RESULT 4 PCT-US95-04258-6

Sequence 6, Application PC/TUS9504258  
 GENERAL INFORMATION:  
 APPLICANT: A DNA MOLECULE ENCODING A MAST CELL  
 TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 STREET: BROWDY AND NEIMARK  
 CITY: Washington Street, N.W., Suite 300  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-in Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04258  
 FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 109257  
 FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: PRCHT=1 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528

SEQUENCE CHARACTERISTICS:  
 LENGTH: 114 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: protein  
 PCT/US95/04258-6

Query Match 62.8%; Score 651; DB 5; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-64;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 CPNLWNRNGSHCYFSMEKDWNSSILKECADKGSHLTFDNGNLFQBYVGEDFYWIG 134  
 Db 1 CPNLWNRNGSHCYFSMEKDWNSSILKECADKGSHLTFDNGNLFQBYVGEDFYWIG 60

Qy 135 LRDIDGWRWEDGPALSLSISNSVVKCQGTIHRCLGHASSCEVALQWICKEKVL P 188  
 Db 61 LRDIDGWRWEDGPALSLSISNSVVKCQGTIHRCLGHASSCEVALQWICKEKVL P 114

RESULT 5  
 US-09-531-056A-23  
 Sequence 23, Application US/09531056A  
 Patent No. 6455683  
 GENERAL INFORMATION:  
 APPLICANT: Bristol-Myers Squibb Company  
 TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI  
 FILE REFERENCE: DB20  
 CURRENT APPLICATION NUMBER: US/09/531,056A  
 CURRENT FILING DATE: 2000-03-20  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 23  
 LENGTH: 76  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-531-056A-23

Query Match 26.4%; Score 273; DB 4; Length 76;  
 Best Local Similarity 59.7%; Pred. No. 1.4e-22;  
 Matches 43; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Qy 75 CPNLWNRNGSHCYFSMEKDWNSSILKECADKGSHLTFDNGNLFQBYVGEDFYWIG 134  
 Db 3 CPDRWKYGRHCCYYVEEKDWNSSLEFCCLARDSHLVITDNOENSLLQVLESEARCWIG 62

Qy 135 LRDIDGWRWEG 146  
 Db 63 LRNMGSRWEDG 74

RESULT 6  
 PCT-US93-10418-2  
 Sequence 2, Application PC/TUS9310418  
 GENERAL INFORMATION:  
 APPLICANT: Ziegler, Steven F.  
 APPLICANT: Harrild, Kathryn A.  
 TITLE OF INVENTION: Activation Antigen CD69  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZTP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/10418  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seese, Kathryn A.  
 REGISTRATION NUMBER: 32,172  
 REFERENCE/DOCKET NUMBER: 2610-WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 233-0644  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US93-10418-2

Query Match 17.8%; Score 184.5; DB 5; Length 199;  
 Best Local Similarity 26.3%; Pred. No. 2.4e-12;  
 Matches 41; Conservative 30; Mismatches 76; Indels 9; Gaps 4;

Qy 35 VSYIMMVAQLGLTILMSLLYQPTLCCSGSKGFMG--SQCSRSPNLMWRNGSHCYFSM 91  
 Db 45 VMNVFTILILIALTALSYQYN--CPEQYTFMSPSDSHVSSCEDWVGYQRKCYFIST 101

Qy 92 EKRDWNSSLKECADKGSHLTFDNGNLFQBYVGEDFYWIGLDGS--WRWEDGPAL 149  
 Db 102 VKRSTWQAQNACSGATAVIIDSKEKDQFLKAYGREENHWGKKEFQHPWWKWSNGKEF 161

Qy 150 SLSIISNSVYQKCGTHRCGLHASSEVALQWICKEK 185  
 Db 162 N-NWFNTVGSDDKCVFLRNTEVSSMCERNLYWICNK 196

RESULT 7  
 US-08-772-440-13  
 Sequence 13, Application US/08772440  
 ; Patent No. 6046158

GENERAL INFORMATION:  
 APPLICANT: Ariizumi, Kiyoshi  
 APPLICANT: Takashima, Akira  
 TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
 TITLE OF INVENTION: LECTINS, DECINT-1 AND DECINT-2, COMPOSITIONS AND USES  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/772,440  
 FILING DATE: CONCURRENTLY HEREWITH  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, David L.  
 REFERENCE/DOCKET NUMBER: 32,165  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 512/418-3000  
 TELEFAX: 512/414-7577  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 199 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-772-440-13

Query Match 16.9%; Score 175.5; DB 3; Length 199;  
 Best Local Similarity 26.2%; Pred. No. 2.3e-11; Indels 43; Gaps 11;  
 Matches 53; Conservative 32; Mismatches 74;

QY 7 YSTLELPAAAPRVQD----DSRKVKAVLHPRCPVSYLVMVALGIL--TVILMSLLYQR 58  
 Db 20 FSTGDHKPRPGSKGSRAFPSSP----RP----TAVENGILCPVVVVVAAVL--- 64

QY 59 TLCCGSRGPMCSQCSRPNLWMRNGSHCYFSMKEKDNSSLKPCADKGSHLTFPDNQG 118  
 Db 65 ----GALGGFSQSC-LPN-WIIGKSCYLFSFGNSWYGSKRHSQGAHLKIDNSKE 117

QY 119 VNLFOQEYVG--DFYWIGL--RDIDG-WRWEDEPA----LSSILSNSVYQCGTI 165  
 Db 118 FEFTESQTSHRNIAFWIGLRSNOSEGPPWFEDSAFFNSFQVRNTVTPQESLILHNQCVWI 177

QY 166 HRCGUHASCEVALQICBKVL 187  
 Db 178 HGSPVYNNQICNTSYSICKEL 199

RESULT 8  
 US-09-247-155-97  
 Sequence 9, Application US/09247155A  
 ; General Information:  
 ; Applicant: Dumas Milne Edwards, Jean-Baptiste  
 ; Applicant: Duciert, Aymeric  
 ; Applicant: Bouquelert, Lydie  
 ; Title of Invention: Complementary DNAs  
 ; File Reference: GENEST.021A  
 ; Current Application Number: US/09/247,155A  
 ; Filing Date: 1999-02-09  
 ; Earlier Application Number: 60/074,121  
 ; Earlier Filing Date: 1998-02-09

GENERAL INFORMATION:  
 EARRIER APPLICATION NUMBER: 60/081,563  
 EARLIER FILING DATE: 1998-04-13  
 EARRIER APPLICATION NUMBER: 60/096,116  
 EARLIER FILING DATE: 1998-08-10  
 EARRIER APPLICATION NUMBER: 60/099,273  
 EARLIER FILING DATE: 1998-10-04  
 NUMBER OF SEQ ID NOS: 182  
 SOFTWARE: Patent-pm  
 SEQ ID NO: 97  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: SIGNAL  
 LOCATION: -47..-1  
 US-09-247-155-97

Query Match 16.9%; Score 175.5; DB 4;  
 Best Local Similarity 26.9%; Pred. No. 2.8e-11; Indels 51; Gaps 12;  
 Matches 61; Conservative 32; Mismatches 83;

QY 1 MADNSISSTLEL---PAAPRVDODSR--WKVKA-VLHRPCVSYLVMVALGILTVLMS 52  
 Db 1 MQEDGYTTLNKTTRKDVLVSGPASSEFWWRVMAILILCVCYGMVGLVALTWSMQRN 60

QY 53 LLLYQRTLCCGS-----KG-FMCSCQCSRCPNLWMRNGSHCYFSMKEK 93  
 Db 61 YLDENENRRTGTLQLAKRFCQYYVKQSELKETFKGHKCSPTCDTNWYGDSCYGFRRHN 120

QY 94 RDWNSSLKFCADGSHLTFPDNQGYNLFQEYVGEDFY---WTGL--RDIDGWRWEDEP 147  
 Db 121 LTWBESKOYCTDMNATLJKI-DRNJ --VEYIKARTHLIRWGLSRSQKSNEWTKWEDG- 175

QY 148 ALSLSILSNSVYQ-----KCGTTHRCGUHASCEVALQICBK 185  
 Db 176 ---SVSENMFELDGGKNNMCAYFHNGKMPHTCENKHYIMCER 218

RESULT 9  
 US-09-531-056A-6  
 Sequence 6, Application US/09531056A  
 ; Patent No. 6455683  
 GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLX PROTEINS AND THEIR SOLUBLE FUSION PROTEINS  
 ; FILE REFERENCE: DB20 NP  
 ; CURRENT APPLICATION NUMBER: US/09/531,056A  
 ; CURRENT FILING DATE: 2000-03-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 191  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-531-056A-6

Query Match 16.8%; Score 174.5; DB 4;  
 Best Local Similarity 25.8%; Pred. No. 2.8e-11; Indels 25; Gaps 6;  
 Matches 48; Conservative 29; Mismatches 84;

QY 11 ELPAPRVDSSRWNKVKAVLHPRCPVSYLVMVALGILTVLMSL--LYQRTLCGGSQF 68  
 Db 15 ELPAPNPGCLHSKHSIRATL----INFLFLMFLMTLIVCNVAALSFAIRNCHOEBSV 69

QY 69 CSQCSRCPNLWMRNGSHCYFSMKEKDNSSLKPCADKGSHLTFPDNQGVNFQEQYVG 128  
 Db 70 CLQAA-CPESWIGFQORKCFYSDDTKWNTSSQFDSDQADLJQVESQDQLNELLRYKCP 128

QY 129 DFYWIGLIRDIDG-WRWEDEP-----PALSLISLSNSVYQCKTIRHGLHAASCEVAL 179  
 Db 129 SDHMIGLSREQQQFWKQWINGTENTRQFPLGAG-----ECAYLINDKGASSARHYTER 180

Qy 180 QWICBK 185  
Db 181 KWICSK 186

RESULT 10  
US-08-738-462-2

Sequence 2, Application US/08738462

GENERAL INFORMATION:  
Patent No. 5965401  
APPLICANT: Chang, Chiwen L.  
APPLICANT: Phillips Jr., Joseph H.  
TITLE OF INVENTION: Purified Mammalian NK Antigens and  
NUMBER OF SEQUENCES: 2  
TITLE OF INVENTION: Related Reagents  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
CITY: Lanier, Lewis L.  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1., Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/738,462  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,435  
FILING DATE: 16-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0397

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-552-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 225 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-738-462-2

Query Match 16.4%; Score 169.5; DB 2; Length 225;  
Best Local Similarity 26.1%; Pred. No. 1.2e-10;  
Matches 59; Conservative 32; Mismatches 84; Indels 51; Gaps 11;

Qy 1 MADNSIYSTLEP-----AAPR YQDDSRWKVAVLHRPC--VSYLYMVALGL 46  
Db 1 MDQQAYAELNLPTSGPESSSSPSLPRDYCGSPWH-QFALKLSCAGILLLVVVTG-L 58

Qy 47 TVILMILLYQRTLCCGSKGFMCSQCS-----RCPNLWMRNGSHCYF 89  
Db 59 SVSVTSLI--QKS-----SIEKCSVDIQQRNKTTERPGLLNCPIWQQLREKCLLF 108

Qy 90 SMEKRDWNSSLRKFCADKGSHLLTFPDNOGYNLFOEYVGED--FYWIGLR--DIDGWRIE 144  
Db 109 SHTVPWNNSLADCSKESSLILLRDKDELINTQNLLRIRKAILFWIGNFSLSEKNWKI 168

Qy 145 DGPALS--LSILSNSSVVKQCGTIIHRCGHASSCEVALQWICRYVL 187  
Db 169 NGSFINSNDLIERGDAKENSCTISQTSYSEYCSSTEWRICQKL 214

RESULT 12  
US-08-722-126A-8

Sequence 8, Application US/08722126A

GENERAL INFORMATION:  
Patent No. 603427  
APPLICANT: PECHT, Israel  
APPLICANT: GUTTMANN, Marcelo D.

TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington

RESULT 11  
PCT-US94-07587-2

STATE: D.C.  
 COUNTRY: UNITED STATES OF AMERICA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0,  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/722,126A  
 FILING DATE: 08-APR-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04258  
 FILING DATE: 06-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 109257  
 FILING DATE: 08-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: PECHT=1A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 115 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-722-126A-8

Query Match 16.1%; Score 166.5; DB 3; Length 115;  
 Best Local Similarity 27.4%; Pred. No. 1..le-10;  
 Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

Qy 75 CPNLWMRNGSHCYFSMEKRDWNSSLKFCAKGSHLTFPDNQGVNLFOEYGFDFWIG 134  
 Db 1 CSEDWVGQRKCYFISTVRSWTAQNACSERGATLAVIDSEKDNNFLKRYAGREHFHWG 60

Qy 135 LRDDG--WRWEDGPALSLSILSNSVVKCGT1HRCGLHASCEVALQWICER 185  
 Db 61 LKKEPGHMKWSNGKEFN-NWFNVTGSDKCVFLKNTEVSSMECTNLYWICNK 112

RESULT 13  
 PCT-US95-04258-B  
 Sequence 8, Application PC/TU95/04258  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
 ; FUNCTION-ASSOCIATED ANTIGEN (MFA)  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0,  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04258  
 ; FILING DATE: 06-APR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 109257  
 ; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: PECHT=1 PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 115 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 PCT-US95-04258-B

Query Match 16.1%; Score 166.5; DB 5; Length 115;  
 Best Local Similarity 27.4%; Pred. No. 1..le-10;  
 Matches 31; Conservative 22; Mismatches 57; Indels 3; Gaps 2;

Qy 75 CPNLWMRNGSHCYFSMEKRDWNSSLKFCAKGSHLTFPDNQGVNLFOEYGFDFWIG 134  
 Db 1 CSEDWVGQRKCYFISTVRSWTAQNACSERGATLAVIDSEKDNNFLKRYAGREHFHWG 60

Qy 135 LRDDG--WRWEDGPALSLSILSNSVVKCGT1HRCGLHASCEVALQWICER 185  
 Db 61 LKKEPGHMKWSNGKEFN-NWFNVTGSDKCVFLKNTEVSSMECTNLYWICNK 112

RESULT 14  
 US-09-127-946-14  
 ; Sequence 14, Application US/09127946  
 ; Patent No. 6416973  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bakker, Alexander B.H.  
 ; APPLICANT: Phillips, Joseph H.  
 ; APPLICANT: Lamier, Lewis L.  
 ; TITLE OF INVENTION: Mammalian Cell Membrane Proteins;  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: DNAX Research Institute  
 ; STREET: 901 California Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/127-946  
 ; FILING DATE: 31-JUL-1998  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/089,168  
 ; FILING DATE: 12-JUN-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/069,692  
 ; FILING DATE: 16-DEC-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/069,639  
 ; FILING DATE: 15-DEC-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/063,717  
 ; FILING DATE: 29-OCT-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/054,430  
 ; FILING DATE: 01-AUG-1997  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P. 34, 090  
 REGISTRATION NUMBER: DX0763X  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 852-0196  
 TELEFAX: (650) 496-1200  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 190 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-127-946-14

Query Match 16.1%; Score 166.5; DB 4; Length 190;  
 Best Local Similarity 24.3%; Pred. No. 2.1e-10;  
 Matches 45; Conservative 31; Mismatches 66; Indels 43; Gaps 5;

QY 40 MVALGILTVL----MSLLYQRTLCGSRGFMCSQC-----72  
 Db 5 MIISGVIVVILKIVGMTEFLYIYPQFKENDGYPTESYGTTSQVNQSOIFGRNDESM 64

QY 73 ----SRCPNLWMRNGSHCYFSMEKRDNNSLKFCADKGSHLTFPDNQGVNLFOEYV 126  
 Db 65 PTRSYGTVCPRNWDHQKCFFFPSSESPWKSDMDCATQSTLAVNPBKLYQLDIA 124

QY 127 GEDFTWIGLRLIDG--WRMEDGPALSLSLNSNVQKCTTHRCGL---HASSCEVAL 179  
 Db 125 GIENTFIGLVRQPGEKKWNRWINNSVNGNTQNQDNFDDCVTYI--GLTKTYDAASCEVSY 181

QY 180 QWICE 184  
 Db 182 RWICE 186

RESULT 15  
 US-09-111-470-10  
 Sequence 10, Application US/09111470  
 Patient No. 6277959

GENERAL INFORMATION:  
 APPLICANT: Valladeau, Jenny  
 APPLICANT: Ravel, Odile  
 APPLICANT: Bates, Elizabeth E.M.  
 APPLICANT: Ford, John  
 APPLICANT: Saeland, Sem  
 APPLICANT: Lebecque, Serge J.E.  
 TITLE OF INVENTION: Mammalian Membrane Protein Genes;  
 TITLE OF INVENTION: Related Reagents  
 NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNA Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/111,470  
 FILING DATE: 08-JUL-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/053, 080  
 FILING DATE: 09-JUL-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34, 090  
 REFERENCE/DOCKET NUMBER: SF0695  
 TELECOMMUNICATION INFORMATION:

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A;Residues: 1-156 <MIL>  
 A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1  
 A;Experimental source: clone cB12  
 C;Genetics:  
 A;Gene: Bluc  
 A;Map Position: 16  
 A;Introns: 17/1; 74/3; 110/2

Query Match 16.2%; Score 166; DB 2; Length 156;  
 Best Local Similarity 29.7%; Pred. No. 2.3e-08;  
 Matches 46; Conservative 19; Mismatches 68; Indels 22; Gaps 5;  
 Qy 42 TGLLITAVLISLYLQVILCGNSNNYSTACSPSCPDRWMKYGHNHYCYSVEEKDNNSLE 101  
 Db 6 TVLILITAVAFAVQAFO-----PHRQPQAQCPDWWIGRKCYFSEDESNTWSSN 56  
 Qy 102 FCLARDSHLLVITDNOEMSLLQVFLSEAFCMGLRNNNS--GWRWEDGSPLNFERSISSLNS 158  
 Db 57 NCSALGDSLAVEDSAELSFPTMWHKCSSPHWVGLSREGKEHPWEWVNRSPL-----SHL 110  
 Qy 159 F-VQ---TCGATINKGQIQLQASSECVPLHGVCKVRL 189  
 Db 111 FQVQGDLCAVLGDAGLSSSHCSTRNWVCTKTPAL 145

RESULT 3  
 WMVZ2

hepatitis lectin homolog (BamHI-CRF2) - fowlpox virus (isolate HP-438 [Munich])  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 16-Jun-2000  
 C;Accession: B29963  
 R;Tomley, F.; Banns, M.; Campbell, J.; Boursnell, M.  
 J. Gen. Virol. 69, 1025-1040, 1988

A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox  
 A;Reference number: J0442; MUID:88229622; PMID:2836548  
 A;Accession: B29963  
 A;Molecule type: DNA  
 A;Residues: 1-167 <RCM>  
 A;Cross-references: GB:D00295; NID:9221380; PIDN:BAA00192.1; PID:9221383  
 C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology  
 F;49-152;Domain: C-type lectin homology <LCN>

Query Match 15.0%; Score 153.5; DB 1; Length 167;  
 Best Local Similarity 25.8%; Pred. No. 3.7e-07;  
 Matches 39; Conservative 29; Mismatches 74; Indels 9; Gaps 5;  
 Qy 36 SCLVATAITGLLTAVLISLYLQWILCGSNYTCASPSCPDRWMKYGHNHYCYSVEEKD 95  
 Db 13 SCYATVTLGLLILPFLTVV-WTCKW-YTAFFPSKVCDEWIGNSKCYYFTINETN 69  
 Qy 96 WNSSLFCLARDSHLLVITDNOEMSLLQVFLSEAFWVGLRNNSGWRWEDGSPLNFERSI 155  
 Db 70 WNDSSKKLCDVMDSSLFLFDNFTETLNFSVRYGRGSY-WIDINQ---INFSLYY 123

RESULT 4  
 T28140

natural killer cell receptor homolog - chicken (fragment)  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T28140  
 R;Mine, S.; Kaufman, J.; Beck, S.  
 Submitted to the EMBL Data Library, May 1998  
 A;Description: DNA sequencing and analysis of the chicken major histocompatibility comp1  
 A;Reference number: 220475  
 A;Accession: T28140  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA

A;Residues: 1-170 <MIL>  
 A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1  
 A;Experimental source: clone cB12  
 C;Genetics:  
 A;Gene: BNK  
 A;Map Position: 16  
 A;Note: Intron positions not resolved (incomplete sequence)  
 Query Match 14.6%; Score 149; DB 2; Length 170;  
 Best Local Similarity 28.6%; Pred. No. 9.9e-07;  
 Matches 34; Conservative 16; Mismatches 67; Indels 2; Gaps 2;  
 Qy 70 ASCPSCPDRWMKYGHNHYCYSVEEKDNNSLEFCLARDSHLLVITDNOEMSLLQVFLSEA 129  
 Db 45 AACLLCQPFQEWLGPCYSTEKEVQDFQYCEHDFLHQGMAGAE 104  
 Qy 130 FCWIGHL-NNSGWRWEDGSPLNFERSISSLNSFVQT-CGATINRNGLQASSCEVPLHGVCKK 186  
 Db 105 PVWIGLEVSINQWVWDNSSYNSTRSDNLSSYMEERGTFRNTKVBDVCSGEHFWVYQCK 163  
 RESULT 5  
 PC7027  
 aggrecan alpha chain - Malayan pit viper (fragment)  
 C;Species: Calloselasma rhodostoma (Malayan Pit Viper)  
 C;Accession: PC7027  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000  
 C;Accession: PC7027  
 R;Chung, C.H.; Au, L.C.; Huang, T.F.  
 Biochem. Biophys. Res. Commun. 263, 723-727, 1999  
 A;Title: Molecular cloning and sequence analysis of aggrecan, a collagen-like platelet  
 A;Reference number: PC7027; MUID:99443731; PMID:10512747  
 A;Accession: PC7027  
 A;Molecule type: mRNA  
 A;Residues: 1-144 <CHU>  
 A;Experimental source: venom gland  
 C;Superfamily: tetranectin; C-type lectin homology  
 C;Keywords: disulfide bond; platelet aggregation; venom  
 Query Match 14.0%; Score 143.5; DB 2; Length 144;  
 Best Local Similarity 29.6%; Pred. No. 2.7e-06;  
 Matches 34; Conservative 17; Mismatches 49; Indels 15; Gaps 4;  
 Qy 68 TCASCPSCPDRWMKYGHNHYCYSVEEKDNNSLEFCLARD-SHLLVITDNOEMSLLQVFL 125  
 Db 6 TRAGLEDCDPWFPSYDQYCFQAFNEKFRQAGNHAASIEADEVPSVWL 65  
 Qy 126 LS-----EAPFCWIGLR----NNSGWRWEDGSPLNFERSISSLNSFVQTCCAINK 168  
 Db 66 ISQKDELADEDYVWIGLRAQNKEQQCSSENSDGSSVSYENL-IDLHHTKKCGALEK 119  
 RESULT 6  
 JC7135  
 agkisacutacin beta chain precursor - sharp-nosed viper  
 N;Alternate names: fibrinogenlytic venom protein  
 C;Species: Agkistrodon acutus (sharp-nosed viper)  
 C;Accession: JC7135; PC7038  
 R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.  
 Biochem. Biophys. Res. Commun. 265, 530-535, 1999  
 A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom  
 A;Reference number: JC7134; MUID:20025379; PMID:10558903  
 A;Accession: JC7135  
 A;Molecule type: mRNA  
 A;Residues: 1-146 <CHE>  
 A;Cross-references: GB:AP176421  
 A;Experimental source: venom gland  
 A;Accession: PC7038  
 A;Molecule type: protein  
 A;Residues: 24-59-83-102-107-112-114 <CH2>  
 C;Superfamily: tetranectin; C-type lectin homology  
 C;Keywords: disulfide bond; heterodimer; venom  
 F;1-23/Domain: signal sequence #status predicted <SIG>

F:24-146/Product : agkisacutacin beta chain #status experimental <MAT>

Query Match 13.9%; Score 142.; DB 2.; Length 146;  
Best Local Similarity 25.0%; Pred. No. 3. 9e-06;  
Matches 42; Conservative 21; Mismatches 55; Indels 50; Gaps 8;

QY 39 VAITLGLITAVILSVLVQWILCQGSNYSCTACSPCPSCPDAMKYGHNHCYFSSVEEKDWN 98  
Db 5 IFVSGFLNLIVFL ----- SLSGTAADCEPSEWSYEGHCKPDEPKWAD 48

QY 99 SLEFCLAA-RDSHLVITDNOE ---MSLQLQVLFSEAFWIGHR---NNSGKRWEEDGSP 149  
Db 49 AEKFCQTQHKGSHLASPHSEEADEFVFLTTPLKTDLWVHKNITNGCYKWKSDTKL 108

QY 150 NF -----SRISNSNSPV-QTCGAIINNSQLOASCSCEVPLHGVK 185  
Db 109 DTKDWREQFECLVSVRTVNNEWLMSMDCG-----TFCSF---VCK 143

RESULT 7

S29822 pancreaticitis-associated protein - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C;Accession: S29822  
R;Itoh, T.; Teraoaka, H.  
B;Itoh, T.; Teraoaka, H.  
A;Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homolog  
A;Reference number: S29821; MUID:93176807; PMID:7679928  
A;Accession: S29822  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Cross-references: GB:ID13509; NID:9286106; PID:BA002727.1; PID:g286107  
C;Superfamily: tetranectin C-type lectin homology <LCH>  
F:40-171/Domain: C-type lectin homology <LCH>

Query Match 13.4%; Score 137.5; DB 2.; Length 175;  
Best Local Similarity 25.7%; Pred. No. 1. 2e-05;  
Matches 46; Conservative 28; Mismatches 70; Indels 35; Gaps 9;

QY 33 PSCSCLVATLGLITAVILSVLVQWILCQGSNYSCTACSPCP---SCPDAMKYGHNHCY 88  
Db 3 PPACSV-----MSWMILLSCUM---LLSQVQGEDSLKRNIPSARISCPKGSDAYGSTCYA 53

QY 89 FSYKEEKDNSSLFCLAR-DSHLIVITDNOEMLQVFL---SEAFCWIGR---- 136  
Db 54 LFQIPQTWDAELACQREGGHLVSVLNSAEEAFLSSMVKRTGNSYQTYWIGHLDPTIGA 113

QY 137 -NNSGNRWEEDGSPLNFSRISNSPVQT---CGAINK---QASSCEVPLHGVCK 185  
Db 114 EPNGGGNEWNSNDYMNIFPNWERNPSTALDRAFGSLSRSAGFLKWRDMTCEVKLPPVCK 172

RESULT 9

A34313 antifreeze protein II precursor - sea raven  
N;Alternate names: pro-antifreeze protein type II  
C;Species: Hemitrichopus americanus (sea raven)  
C;Accession: A34313; A24602; PC2386; PC2387; S65733  
R;Hayes, P.H.; Scott, G.K.; Ng, N.F.L.; Hew, C.L.; Davies, P.L.  
J. Biol. Chem. 264, 18761-18767, 1989  
A;Title: Cystine-rich type II antifreeze protein precursor is initiated from the third  
A;Reference number: A34313; MUID:90036986; PMID:2572595  
A;Accession: A34313  
A;Molecule type: DNA; mRNA  
A;Residues: 1-37, G, 39-163 <HAY>  
A;Cross-references: GB:J05100; NID:9213875; PID:AAA49618.1; PMID:9213876  
A;Note: there are 12-15 copies in the genome; the sequence of SR was determined  
A;Title: parts of this sequence, including the amino end of the mature protein, were determined  
A;Note: the amino end of the mature protein is blocked  
R;Ng, N.F.; Trinh, K.Y.; Hew, C.L.  
J. Biol. Chem. 261, 15690-15695, 1986  
A;Title: Structure of an antifreeze polypeptide precursor from the sea raven, Hemiript  
A;Reference number: A24602; PMID:87057207; PMID:3782083

RESULT 8

A28351 pancreaticitis-associated protein precursor - rat  
N;Alternate names: lithostathine  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 11-May-2000  
C;Accession: A28351; A39081; PL0147; S34618  
R;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Okamoto, J. Biol. Chem. 263, 2111-2114, 1988  
A;Title: A novel gene activated in regenerating islets.  
A;Reference number: A92704; MUID:88115343; PMID:296300  
A;Accession: A28351  
A;Molecule type: mRNA  
A;Residues: 1-165 <TER>  
A;Cross-references: GB:MI8962; NID:9206604; PID:AAA42028.1; PID:9206605  
R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagon, J.C.; Giorgi, D.  
J. Biol. Chem. 266, 786-791, 1991  
A;Title: Rat pancreatic stone messenger RNA: Abundant expression in mature exocrine  
A;Reference number: A39081; MUID:91093273; PMID:1985964



|   |   |
|---|---|
| A; Reference number: A5313  | A; Accession: A49616  |
| A; Status: not compared with conceptual translation   | A; Molecule type: DNA   |
| A; Molecule type: DNA   | A; Residues: 1-175 <DUS2>   |
| A; Cross-references: GB:L07127; NID:9349550; PID:AAA41805_1; PMID:9349551   | A; Cross-references: GB:L15533; NID:9482908; PID:AAA60020_1; PMID:9482909   |
| A; Note: an incorrect initiation codon was used   | R; Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C.   |
| A; Reference number: 151899; PMID:8238345   | Cancer Res. 52, 5089-5095, 1992   |
| A; Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is expressed in rat  | A; Title: A novel gene (HIP) activated in human primary liver cancer.   |
| A; Status: preliminary; translated from GB/EMBL/DDJB  | A; Reference number: A49311   |
| A; Molecule type: mRNA  | A; Accession: A49311  |
| A; Residues: 1-175 <ITO>  | A; Molecule type: mRNA  |
| A; Cross-references: GB:M98049; NID:933210; PID:AAA16341_1; PMID:9254695  | A; Residues: 1-175 <LA2>  |
| A; Note: in Genbank entry RATPAPC, release 113.0, the source is designated as Rattus rattus   | A; Cross-references: GB:D13510; NID:9285970; PID:BAA02728_1   |
| R; Iovanna, T.; West, C.; Beutler, E.   | R; Iovanna, J.; Orelle, C.; Keim, V.; Masciotta, L.; Dagorn, J.C.; Iovanna, J.L.  |
| Gene 18, 290-300, 1992  | Eur. J. Biochem. 224, 29-37, 1994   |
| A; Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.  | A; Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in a human gene (HIP/PAP)                             |
| A; Reference number: JC1257; MUID:92380521; PMID:1511905  | A; Reference number: S48197; PMID:94357229; PMID:8076648  |
| A; Accession: JC1257  | A; Accession: S48197  |
| A; Molecule type: mRNA  | A; Status: preliminary  |
| A; Residues: 1-6 'S', 8-175 <KAM>   | A; Molecule type: mRNA  |
| A; Cross-references: GB:S43715; NID:9254694; PID:AA2B23103_1; PMID:9254695  | A; Residues: 1-175 <LA2>  |
| R; Iovanna, J.; Orelle, C.; Keim, V.; Dagorn, J.C.  | R; Orelle, B.; Keim, V.; Masciotta, L.; Dagorn, J.C.; Iovanna, J.L.   |
| J. Biol. Chem. 266, 2464-2469, 1991   | R; Clin. Invest. 90, 2284-2291, 1992  |
| A; Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a   | A; Title: Human pancreatitis-associated protein. Messenger RNA cloning and expression in a human gene (HIP/PAP)                             |
| A; Reference number: A41719   | A; Reference number: 155580; PMID:93107309; PMID:14463087   |
| A; Accession: A41719  | A; Status: preliminary; translated from GB/EMBL/DDJB  |
| A; Molecule type: mRNA  | A; Cross-references: GB:S511768; NID:9262368; PID:AAH24642_1; PMID:9262369  |
| A; Cross-references: GB:M55149; NID:9206030; PID:AAA41807_1; PMID:9206031   | A; Residues: 1-175 <RES>  |
| A; Note: the amino-terminal residue of the mature protein was identified as Glu   | A; Cross-references: GB:136839; OMIM:167805   |
| A; Gene: pap  | A; Gene: GDB:PAP; HIP   |
| A; Introns: 26/1; 65/3; 111/3; 154/1  | A; Map Position: 2p12-2p12  |
| C; Superfamily: Y; retranscritin; C-type lectin homology  | A; Map Position: 2p12-2p12  |
| C; Keywords: lectin; pancreas   | C; Superfamily: tetranectin; C-type lectin homology   |
| F; 1-26/Domain: signal sequence #status predicted <SIG>   | C; Keywords: acute phase; extracellular protein; pancreas   |
| F; 40-175/Domain: C-type lectin homology <LCH>  | F; 1-26/Domain: signal sequence #status predicted <SIG>   |
| F; 40-51; 68-171; 146-163/disulfide bonds: #status predicted  | F; 27-175/Domain: C-type lectin homology <LCH>  |
| Db 9 VMWMMQLM--LLSQVQEDSPPKI PSARISCPKSSQAYSYCYALFQQTWFAE 65  | F; 40-51; 68-171; 146-163/disulfide bonds: #status predicted  |
| Query Match Score 13.0%; DB 2; Length 175;  | Query Match Score 12.8%; DB 2; Length 175;  |
| Best Local Similarity 25.1%; Pre. No. 3.6e-05;  | Best Local Similarity 26.0%; Pre. No. 5.6e-05;  |
| Matches 42; Conservative 28; Mismatches 68; Indels 29; Gaps 7;  | Matches 46; Conservative 25; Mismatches 71; Indels 35; Gaps 8;  |
| Qy 45 LLTAVLLSTYLQWLQCLQQSNYSTCASCP---SCPDRWMKGNHCYYSVERKDWNSSL 100   | Qy 38 IVAITIGHLTAVLLSLLYQWLQCLQQSNYSTCASCP---CPDRWMKGNHCYYSVEE 93   |
| Db 66 LACOKRPECHLVSVLNARAPASFLASMVNTGNSYQYTWTGLHDPTLGGEPNGGGWENSN 125   | Db 2 LPPMAlPVSVMILSCIM--LILSOVQGEPEORELPASARIICPKGSKAYGSHCYALPLSP 58  |
| Qy 147 SPNFSRISNSNPFQTL---CGAINKNG---LQASSCEVPLHGVCK 185  | Qy 94 KDWNSLSEFLCLARDS-HILVITDNQNSLQVFL---SEAFCWIGR-----NNS 139   |
| Db 126 DINYVNVNERNPSTALDRFCGSGLSRSQSSFLWRDTTCVKLPVCK 172  | Db 59 KSWTDADIAQCRPSGNIUVSVLGAESFVVSKLGSIGNSYVWGLHDPTQGTENGGE 118   |
| RESULT 13   | Qy 140 GMRWEDGSPLNF----SRISSNSFVQTCGAINKNG---QASSCEVPLHGVCK 185   |
| A49616  | Db 119 GNEWSSSDVMNYFAWERNPSTISSPGH--CASLRSRSTAFLRWKDNINCNRVRLPYVCK 172  |
| pancreatitis-associated protein precursor - human   | C; Species: Homo sapiens (man)  |
| N; Alternative names: C-type lectin; pancreatic stony protein homolog HIP   | C; Accessions: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 21-Jul-2000  |
| C; Species: Homo sapiens (man)  | R; Iovanna, T.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.   |
| C; Accession: A49616; A49311; S29121; S48197; T55580  | Geonomics 19, 108-114, 1994   |
| R; Iovanna, J.L.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.   | A; Title: Molecular cloning, genomic organization, and chromosomal localization of the human B4A3-2 precursor - barnacle (Megabalanus rosa) |
| A; Title: Molecular cloning, genomic organization, and chromosomal localization of the human B4A3-2 precursor - barnacle (Megabalanus rosa) | C; Species: Megabalanus rosa  |
| A; Reference number: A49616; PMID:94245143;   | C; Reference number: A49616; PMID:8188210   |

C;Date: 31-Dec-1988 #sequence\_revision 09-Sep-1994 #text\_change 16-Jul-1999  
 C;Accession: JC1504; A26094  
 R;Takamatsu, N.; Taira, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, T.  
 Gene 128, 251-255, 1993  
 A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure and  
 A;Reference number: JCI1503; MUID:93292934; PMID:8514190  
 A;Accession: JC1504  
 A;Molecule type: mRNA  
 A;Residues: 1-162 <PAK>  
 R;Muramoto, K.; Kamiya, H.  
 Biochim. Biophys. Acta 874, 285-295, 1986  
 A;Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.  
 A;Reference number: A26094  
 A;Accession: A26094  
 A;Molecule type: protein  
 A;Residues: 25-162 <MR>  
 A;Note: 146-Arg was also found  
 C;Comment: This three Galactose-binding lectin is isolated from the coelomic fluid.  
 C;Comment: This protein plays important roles in defense mechanisms and in development a  
 C;Superfamily: The molecule is a tetramer of identical chains.  
 C;Keywords: tetranectin; C-type lectin homology  
 P;1-24/#Product: signal sequence #status predicted <SIG>  
 P;25-162/#Product: lectin BRA3-2 #status experimental <MAT>  
 P;26-150/Domain: C-type lectin homology <LCH>  
 P;26-39,56-150,125-142/Disulfide bonds: #status experimental  
 P;157/Disulfide bonds: interchain (to 160) #status experimental  
 P;160/Disulfide bonds: interchain (to 157) #status experimental  
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 Best Local Similarity 25.5%; Pred. No. 6.4e-05;  
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 Best Local Similarity 24.8%; Pred. No. 8e-05;  
 Matches 32; Conservative 22; Mismatches 63; Indels 12; Gaps 5;  
 Query Match 12.5%; Score 128.7%; DB 2; Length 146;  
 Best Local Similarity 24.8%; Pred. No. 8e-05;  
 Matches 32; Conservative 22; Mismatches 63; Indels 12; Gaps 5;  
 Qy 67 STCASCSCPSPDRWMKYGNHCCCCYEEKDKNSSLFCLARDS--HLLVLTDNQEMSLI-- 12/2  
 Db 17 SLSGTAADCBDWSSTEGHCKPKSPKNADEAENCTQQHEAGGLHVSFQSEADEVVK 76  
 Qy 123 --QVPLSEAFCWIGIR-- -NNSGMRWEDGSPLNFSRISNSFVQTCGANNKNGQASSC 17/6  
 Db 77 LAFQTEGHSTF-WMGISNTVNQCNWNSNEAMLRYKAWABESYCVYFKSTN-NKVRSRAC 13/4  
 Qy 177 EVPLHGIVCK 18/5  
 Db 135 RMMAQFVCE 14/3  
 Search completed: August 10, 2004, 16:35:20  
 Job time : 18 secs

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RESULT 15  
 JC4691  
 coagulation factor IX/factor X-binding protein chain A precursor - habu  
 C;Species: Trimeresurus flavoviridis (habu)  
 C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Jun-2000  
 C;Accession: JC4691; B39332; JC4330  
 R;Matsuzaki, R.; Yoshihara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.  
 Biochem. Biophys. Res. Commun. 220, 382-387, 1996  
 A;Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from s  
 A;Reference number: JC4690; MUID:96184662; PMID:8645314  
 A;Accession: JC4691  
 A;Molecule type: mRNA  
 A;Residues: 1-146 <MAT1>  
 A;Cross-references: DDBJ:D83332; NID:91402641; PID:BA11888\_1; PID:g1402642  
 A;Experimental source: venom  
 R;Atoda, H.; Hyuga, M.; Morita, T.  
 J. Biol. Chem. 266, 14903-14911, 1991  
 A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate  
 otein, tetranecktin, and lymphocyte Fc epsilon receptor for immunoglobulin E.  
 A;Reference number: B39332; MUID:91332000; PMID:1831197  
 A;Accession: B39332  
 A;Molecule type: protein  
 A;Residues: 24-146 <ATO>  
 R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.  
 J. Biochem. 118, 965-973, 1995  
 A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flav  
 A;Reference number: JC4329; MUID:9618509; PMID:8749314

| Result No. | Score | Query       | Match | Length | DB ID                               | Description |
|------------|-------|-------------|-------|--------|-------------------------------------|-------------|
| 1          | 198.5 | CD94_MACMU  | 179   | 1      | Q9Mzk9 macaca mulatta               |             |
| 2          | 196.5 | CD94_HUMAN  | 179   | 1      | Q13241 homo sapiens                 |             |
| 3          | 194.5 | CD94_PANTR  | 179   | 1      | Q9mz41 pan troglodytes              |             |
| 4          | 156.5 | CLE2_HUMAN  | 17.1  | 149    | P02478 homo sapiens                 |             |
| 5          | 156.5 | V239_FOWEVY | 163   | 1      | P14371 fowlpox virus                |             |
| 6          | 153.5 | V008_FOWEVY | 167   | 1      | P14370 fowlpox virus                |             |
| 7          | 147.5 | PBCG_MESAU  | 175   | 1      | Q92778 mesocercerulus               |             |
| 8          | 147   | PAP3_MOUSE  | 174   | 1      | O09049 mus musculus                 |             |
| 9          | 146   | CHBB_CROHO  | 117   | 1      | P81509 crotalus horridus            |             |
| 10         | 137.5 | PAPI_MOUSE  | 175   | 1      | P15230 mus musculus                 |             |
| 11         | 137   | LITH_RAT    | 165   | 1      | P10758 rattus norvegicus            |             |
| 12         | 136   | IINP_HEMAM  | 163   | 1      | P05140 hemipterus                   |             |
| 13         | 134.5 | LITH_BOVIN  | 175   | 1      | P21332 bos taurus                   |             |
| 14         | 134   | PAP2_MOUSE  | 137   | 1      | O09037 mus musculus                 |             |
| 15         | 134   | MMEB_AGRKHA | 146   | 1      | Q9y199 agkistrodon halophilus       |             |
| 16         | 132.5 | PAP1_RAT    | 175   | 1      | P81531 rattus norvegicus            |             |
| 17         | 132   | CYXB_CRODU  | 12.9  | 148    | P91427 crotalus durissus terrificus |             |
| 18         | 130.5 | PAPI_HUMAN  | 175   | 1      | P06141 homo sapiens                 |             |
| 19         | 129   | LEC3_MEGRO  | 162   | 1      | P07439 megalobalanus                |             |
| 20         | 128   | IXB_TRIFL   | 146   | 1      | P22807 trimeresurus albolabialis    |             |
| 21         | 128   | IXB_HUMAN   | 166   | 1      | P48304 homo sapiens                 |             |
| 22         | 126   | CVXA_CRODU  | 12.5  | 133    | P81397 agkistrodon halophilus       |             |
| 23         | 124   | RHCA_AGRKHA | 12.3  | 133    | P4854 rattus norvegicus             |             |
| 24         | 123.5 | ABA4_TRIAS  | 12.1  | 123    | P22029 bothrops jararacussu         |             |
| 25         | 123   | ABA1_TRIAS  | 12.1  | 133    | P81111 trimeresurus albolabialis    |             |
| 26         | 123   | PLC_HALLA   | 12.0  | 155    | P82396 halictis laevigata           |             |
| 27         | 123   | PAP3_RAT    | 12.0  | 158    | P4854 rattus norvegicus             |             |
| 28         | 122   | BOTB_BOTIA  | 11.9  | 174    | P22030 bothrops jararacussu         |             |
| 29         | 121.5 | ECB2_ECHCA  | 11.9  | 125    | P81996 echis carinatus              |             |
| 30         | 120   | ABA2_TRIAS  | 11.7  | 123    | P81112 trimeresurus albolabialis    |             |
| 31         | 115   | LITA_HUMAN  | 11.2  | 134    | P03451 homo sapiens                 |             |
| 32         | 115   | NKGF_PANTR  | 11.1  | 158    | P95511 pan troglodytes              |             |

| Scoring table: BLOSUM62                            |              | Gapop 10.0 , Gapext 0.5 |       | ALIGNMENTS |   |
|--|--------------|-------------------------|-------|------------|---|
| Scanned:   | 141681 seqs, | 52070155 residues       | 41282 | RESULT 1   | CD94_MACMU STANDARD; PRT; 179 AA.   |
| Total number of hits satisfying chosen parameters: |              |                         |       | ID         | CD94_MACMU STANDARD; PRT; 179 AA.   |
| Minimum DB seq length: 0                           |              |                         |       | AC         | Q9Mzk9; Q9GK91; Q9MKZ7; Q9MZK8;   |
| Maximum DB seq length: 189                         |              |                         |       | DT         | 28-FEB-2003 (Rel. 41, Created)  |
| Post-processing: Minimum Match 0%                  |              |                         |       | DT         | 28-FEB-2003 (Rel. 41, Last sequence update)   |
| Post-processing: Maximum Match 100%                |              |                         |       | DE         | Natural killer cells antigen CD94 (NK cell receptor) (Killer cell)  |
| Database : SwissProt_42::*                         |              |                         |       | DE         | lectin-like receptor subfamily D, member 1).  |
| Scoring table: BLOSUM62                            |              |                         |       | GN         | KURD1 OR CD94.  |
| Gapop 10.0 , Gapext 0.5                            |              |                         |       | OS         | Macaca mulatta (Rhesus macaque).  |
|  |              |                         |       | OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |
|  |              |                         |       | OC         | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;   |
|  |              |                         |       | OC         | Cercopitheciidae; Macaca.   |
|  |              |                         |       | OX         | NCBI_TaxID=9544;  |
|  |              |                         |       | RN         | [1]   |
|  |              |                         |       | RP         | SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).   |
|  |              |                         |       | RX         | MEIDLINE=20322487; PubMed=108666118;  |
|  |              |                         |       | RA         | LaBonte M.L., Levy D.B., Letvin N.I.,   |
|  |              |                         |       | RT         | "Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D."  |
|  |              |                         |       | RT         | RT Immunogenetics 51:496-499 (2000).  |
|  |              |                         |       | RT         | RT Immunogenetics 51:496-499 (2000).  |
|  |              |                         |       | RN         | [2]   |
|  |              |                         |       | RP         | SEQUENCE FROM N.A. (ISOFORM 1).   |
|  |              |                         |       | RX         | MEIDLINE=21158386; PubMed=11261935;   |
|  |              |                         |       | RA         | Kravitz R.H., Grandell R.L., Golos T.G.; "Selective expression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua."   |
|  |              |                         |       | RT         | RT Immunogenetics 53:69-73 (2001).  |
|  |              |                         |       | RL         | FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. SUBUNIT: Can form disulfide-bonded heterodimer with NKG2-family members.  |
|  |              |                         |       | CC         | CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  |
|  |              |                         |       | CC         | CC -1- ALTERNATIVE PRODUCTS: Named isoforms=3;  |
|  |              |                         |       | CC         | CC Name=1; Synonyms=CD9Z9-1; Sequence=Displayed;  |
|  |              |                         |       | CC         | CC IsoID:Q9Mzk9-1; Name=Natural killer cells.   |
|  |              |                         |       | CC         | CC -1- SIMILARITY: Contains 1 C-type lectin family domain. Name=2; Synonyms=CD94-B; Sequence=VSP_003055;  |
|  |              |                         |       | CC         | CC Name=3; Synonyms=CD94 alt; Sequence=VSP_003054;  |
|  |              |                         |       | CC         | CC IsoID:Q9Mzk9-3; Sequence=VSP_003054;   |
|  |              |                         |       | CC         | CC -1- TISSUE SPECIFICITY: Natural killer cells.  |
|  |              |                         |       | CC         | CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  |
|  |              |                         |       | CC         | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |
|  |              |                         |       | DR         | EMBL: AF190331; AAF745271; -;   |
|  |              |                         |       | DR         | EMBL: AF190332; AAF745281; -;   |
|  |              |                         |       | DR         | EMBL: AF190333; AAF745282; -;   |

DR EMBL; AAF74529\_1; -;  
 DR EMBL; AF24886; AAG34498\_1; -;  
 DR HSSP; P22897; JEGG.  
 DR InterPro; IPR01304; Lectin\_C.  
 DR Pfam; PF0059; Lectin\_c\_1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2\_1.  
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin;  
 KW Alternative splicing; Polymorphism.  
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 (POTENTIAL).  
 FT DOMAIN 32 179 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 98 176 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 61 72 BY SIMILARITY.  
 FT DISULFID 89 174 BY SIMILARITY.  
 FT CARBOHYD 152 166 BY SIMILARITY.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 1 34 MAVEKTLMLRISGTLLIICLSLMATHILLKNS -> MA  
 (in isoform 3).  
 FT /FTID=VSP\_003054.  
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 SQ SEQUENCE 179 AA; 20607 MW:  
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 Matches 54; Conservative 24; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAITGLITAVILSVLYQWLQCGSN--YSTOASCSCPDRWMKYGNCYXFVSE 92  
 Db 20 CLSILMA-TLGILKNSFTKLGVPEPAYTPGNIELQKSDCCSCKEWGVRCNYCFISSE 78  
 QY 93 EKDWNSSLEFFCIAQDASHLIVITDNGQEMSLQQYELSAFCWIGL---RNNNSGRWEDGSPL 149  
 Db 79 EKTWNSSRFHCFQASOKSSQLQNRDIDFMS--SSQFYWGLSYSEBTPAWLWNGSAL 136  
 QY 150 NFSRISNSF --- VQTGAAKNGK-LQASSCEVPLHGVCK 186  
 Db 137 --SQYLFPSFETKEPKNCIATNSKGNAELDESCETKNRYICKQ 176

RESULT 2  
 CD94\_HUMAN STANDARD; PRT; 179 AA.  
 AC Q133241; O433221; Q9UBE3; Q9UEQ0;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell  
 DE lectin-like receptor subfamily D, member 1) (RP43).  
 GS KLRD1 OR CD94.  
 GO Homo sapiens (Human).  
 OC Burkartyo; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC NCBI\_TAXID=9605; Lanier L.L.;  
 CX "Molecular characterization of human CD94: a type II membrane  
 RN glycoprotein related to the C-type lectin superfamily.";  
 RP TISSUE=BLOOD;  
 RX MEDLINE=96011848; PubMed=7589107;  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RX TISSUE=Placenta; Primates; Catarrhini; Hominidae; Homo.  
 RN [1] DE Natural killer cells antigen CD94 (NK cell receptor) (Killer cell  
 DE lectin-like receptor subfamily D, member 1) (RP43).  
 RN Phillips J.H., Lopez-Botet M., Carretero M., Lopez-Botet M.,  
 RA Lehrach H., Francis P., Lopez-Botet M.,  
 RA "Structure of the human CD94 C-Type lectin gene.";  
 RT Immunogenetics 47:305-309(1996).  
 RN [3] RPI  
 SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Biassoni R.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4] RPL  
 SEQUENCE FROM N.A. (ISOFORM 3).  
 RP MEDLINE=9267245; PubMed=9601951;  
 RA Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K.,  
 RA Tohma S., Inoue T., Yamamoto K., Juji T.;  
 RT "A alternatively spliced form of the human CD94 gene.";  
 RL Immonogenetics 48:87-88(1998).  
 RN [5] RPN  
 SEQUENCE FROM N.A. (ISOFORM 1).  
 RP TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Scheuer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schuler G.D.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., McDonald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rosa S.S., Loqueland N.A., Peters G.J., Abramson K.J., Millahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bulyk S.W.,  
 RA Villain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heitton E., Kerteman M., Madan A., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shervchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schwartz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,  
 RA Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC !- FUNCTION: Plays a role as a receptor for the recognition of MHC  
 CC class I HLA-E molecules by NK cells and some cytotoxic T-cells.  
 CC !- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family  
 CC members.  
 CC !- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC !- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative\_splicing; Named isoforms=3;  
 CC Name=1; Synonyms=CD94-A;  
 CC Name=2; Synonyms=CD94-1; Sequence=Displayed;  
 CC Isoid=Q13241-1; Sequence=CD94-B;  
 CC Isoid=Q13241-2; Sequence=VSP\_003053;  
 CC Name=1; Synonyms=CD94\_4; alt;  
 CC Isoid=Q13241-3; Sequence=VSP\_003052;  
 CC !- TISSUE SPECIFICITY: Natural killer cells.  
 CC !- SIMILARITY: Contains a C-type lectin family domain.  
 CC !- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".

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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; U30610; AAC50291\_1;  
 DR EMBL; Y14287; CAA74663\_1;  
 DR EMBL; Y14288; CAA74663\_1; JOINED.  
 DR EMBL; AJ000673; CAA04230\_1;  
 DR EMBL; AB009597; BAA24450\_1;  
 DR EMBL; AB010084; BAA24451\_1;  
 DR EMBL; BC028009; AAH28009\_1;  
 DR PDB; 1B6E; 15-JUN-99.

|    |  |          |   |
|----|--|----------|---|
| DR | Genew; HGNC:6378; KLRD1.   | RA       | Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guehlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and NKG2 genes."   |
| DR | MIM: 602894; -.  | RA       | RT  |
| DR | GO; GO:000386; C:plasma membrane; TAS.   | RT       | J Immunol. 168:240-252 (2002).  |
| DR | GO; GO:0004886; F:transmembrane receptor activity; TAS.  | RL       | -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.   |
| DR | GO; GO:0006960; P:antimicrobial humoral response (sensu lamer.); TAS.  | CC       | -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family members.  |
| DR | GO; GO:000166; P:cell surface receptor linked signal transdu. . . ; TAS.   | CC       | -!- SUBCELLULAR LOCATION: Type II membrane protein.   |
| DR | Interpro; IPR01304; Lectin_ C.   | CC       | -!- ALTERNATIVE PRODUCTS:   |
| DR | SMART; SM00034; Lectin_1.  | CC       | -!- Event-Alternative splicing; Named isoforms=2;   |
| DR | PROSITE; PS00615; C TYPE LECTIN_1; FALSE_NEG.  | CC       | Comment=Additional isoforms seem to exist;  |
| DR | PROSITE; PS50041; C TYPE LECTIN_2; 1.  | CC       | Name=1; Synonyms=CD94-A;  |
| KW | Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing; 3D-structure.   | CC       | IsoId=Q9M241-1; Sequence-Displayed;   |
| FT | DOMAIN 1 10 CYTOPLASMIC (POTENTIAL) SIGNAL ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  | CC       | Name=2; Synonyms=CD94-B;  |
| FT | TRANSMEM 11 31 EXTRACELLULAR (POTENTIAL) C-TYPE LECTIN (LONG FORM).  | CC       | IsoId=Q9M241-2; Sequence-VSP 003056;  |
| FT | DOMAIN 32 179 DISULFID 61 72   | CC       | -!- TISSUE SPECIFICITY: Natural killer cells  |
| FT | DISULFID 89 174  | CC       | -!- SIMILARITY: Contains 1 C-type Lectin family domain.   |
| FT | DISULFID 152 166   | CC       | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch). |
| FT | CARBONYD 83 83   | CC       | CC  |
| FT | CARBONYD 132 132   | CC       | CC  |
| FT | VARSPLIC 1 34  | CC       | CC  |
| FT | VARSPLIC 105 105   | CC       | CC  |
| FT | SEQUENCE 179 AA; 20497 MW; 1884D99EBD9583A7 CRC64;   | CC       | CC  |
| SQ | SEQUENCE 179 AA; 20497 MW; 1884D99EBD9583A7 CRC64;   | DR       | EMBL; AF250054; AAF86964; 1; -.   |
| DR | P22897; 1EGG.  | DR       | HSSP; P22897; 1EGG.   |
| DR | InterPro; IPR01304; Lectin_C.  | DR       | InterPro; IPR01304; Lectin_C.   |
| DR | PFAM; PF00059; lectin_c_1.   | DR       | SMART; SM00034; CLECT; 1.   |
| DR | PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.  | DR       | PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.   |
| DR | PS50041; C_TYPE_LECTIN_2; 1.   | DR       | PS50041; C_TYPE_LECTIN_2; 1.  |
| DR | Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing.   | DR       | Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing.  |
| FT | TRANSMEM 1 10 CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  | FT       | TRANSMEM 1 10 CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).   |
| FT | DISULFID 152 166 BY SIMILARITY.  | FT       | DISULFID 152 166 BY SIMILARITY.   |
| FT | CARBONYD 83 83 N-LINKED (GLCNAC. . . ) (POTENTIAL).  | FT       | CARBONYD 83 83 N-LINKED (GLCNAC. . . ) (POTENTIAL).   |
| FT | CARBONYD 132 132 N-LINKED (GLCNAC. . . ) (POTENTIAL).  | FT       | CARBONYD 132 132 N-LINKED (GLCNAC. . . ) (POTENTIAL).   |
| DB | 137 -SQYLFPEEFENTKNCIAYPNQNALDESEDKRYCKQ 176   | FT       | VARSPLIC 105 105 L->LO (in isoform 2).  |
| DB | 137 -SQYLFPEEFENTKNCIAYPNQNALDESEDKRYCKQ 176   | FT       | FTId=vsp 003056 /FTId-vsp 003056  |
| Qy | 93 EKDWNSSLEFLCLARDSHLIVITTDNQENSLLOVLFSEAFWIGL--RNNNSGRMRWEDGSPL 149  | SEQUENCE | 179 AA; 20493 MW; 7244D99EBD9587B7 CRC64;   |
| DB | 79 ORKTNWESRHLCAQSQKSSLQLQNTDELDFMS--SSQQFYWIGL-SYSSEHTAWLWENSSA 136   | Qy       | Query Match 19.0%; Score 194.5; DB 1; Length 179;   |
| DB | 150 NEFRISNSF---VQPTGAINKNG-LQASSCEVPLHGCKK 186  | DB       | Best Local Similarity 32.7%; Pred. No. 1.3e-11;   |
| Qy | 137 -SQYLFPEEFENTKNCIAYPNQNALDESEDKRYCKQ 176   | DB       | Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;  |
| DB | RESULTS 3 CD94_PANTR ID CD94_PANTR STANDARD; PRT; 179 AA.  | Qy       | 35 CSCLVATLGLLTAVLLSVALYQWILQGSN--YSTCASCPSCPDWAKYGNHCTYFSVE 92   |
| AC | 09M241; 28-FEB-2003 (Rel. 41, Created)   | DB       | 20 CLSLMA_TLGILKKNSTKLSTEPATPGPNIELQDSDCSQQEKGYRWEQGSP 149  |
| DT | DT 28-FEB-2003 (Rel. 41, Last sequence update)   | Qy       | 93 EKDWNSSLEFLCLARDSHLIVITTDNQENSLLOVLFSEAFWIGL--RNNNSGRMRWEDGSPL 149   |
| DT | DT 10-OCT-2003 (Rel. 42, Last annotation update)   | DB       | 79 QKTWNESSRHLCAQSQKSSLQLQNTDELDFMS--SSQQFYWIGL-SYSSEHTAWLWENSSA 136  |
| DE | Natural killer cells antigen CD94 (NK cell receptor)   | Qy       | 150 NEFRISNSF---VQPTGAINKNG-LQASSCEVPLHGCKK 186   |
| DE | Natural-like receptor subfamily D, member 1.   | DB       | Xhakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Cooper S.L., Valiante N.M., Lanier L.L., Parham P., "Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans"; Immunity 12:687-698 (2000).   |
| RA | SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE:20350666; PubMed=10894168; Xhakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L., Muir D.G., Cooper S.L., Valiante N.M., Lanier L.L., Parham P., "Rapid evolution of NK cell receptor systems demonstrated by comparison of chimpanzees and humans"; Immunity 12:687-698 (2000). | Qy       | 150 NEFRISNSF---VQPTGAINKNG-LQASSCEVPLHGCKK 186   |
| RN | [2]  | DB       | RA Q92478; Q9UQB4; AC PRT; 149 AA.  |
| RA | ALTERNATIVE SPlicing.  | DB       | DB 137 -SQYLFPEEFENTKNCIAYPNQNALDESEDKRYCKQ 176   |
| RX | MEDLINE=21623889; PubMed=11751968;   | DT       | RESULT 4 CLE2_HUMAN ID CLE2_HUMAN STANDARD; AC PRT; 149 AA.   |





DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW SIGNAL; Lectin. 1. 26 BY SIMILARITY  
 PANCREATIC BETA CELL GROWTH FACTOR.  
 FT CHAIN 27 175 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 38 173 BY SIMILARITY.  
 FT DISULFID 40 51 BY SIMILARITY.  
 FT DISULFID 68 171 BY SIMILARITY.  
 FT DISULFID 146 163 BY SIMILARITY.  
 SQ SEQUENCE 175 AA; 19940 MW; 3854F36RA35D17CE CRC64;

Query Match 14.4%; Score 147.5; DB 1; Length 175;  
 Best Local Similarity 24.6%; Pred. No. 4.1e-07;  
 Matches 42; Conservative 34; Mismatches 72; Indels 23; Gaps 7;

CY 38 LVAITLGLTAVLLSVLY-QWILCGNSNTCASCSPCPDRMMKYGNHCYYSVEKDW 96  
 2 MJPMTLCRMSPMILLSCIMFLWSVGEBSQRKLPSRTCPGSVAYGSYCSLILPQTW 61

QY 97 -NSSLEFCCLARDSHLIVITDQNEMSLQVLFSEA---FCWIGLR-  
 62 SNAELLSQMHEFSGHIAFLLSTGKQVNLQVLTAYQITWIGHDPSHGTLPNGSWMK 142

QY 143 WEDGSPLNFSRISISSLSSNPFVQT---CCAIN-KNGLOA---SSCEVPLHGVCX 185  
 122 WSSNVLTIFTYNWERNEPSSIAADRGYCAVLSQKSFGQKWRDFNCENELPYICK 172

Db DISULFID 174 AA; 19307 MW; 5575E9E56A4D8CEF CRC64;

Query Match 14.4%; Score 147.5; DB 1; Length 174;  
 Best Local Similarity 26.5%; Pred. No. 4.5e-07;  
 Matches 45; Conservative 30; Mismatches 73; Indels 22; Gaps 7;

QY 38 LVAITLGLTAVLLS-VLIQWILCGNSNTCASCSPCPDRMMKYGNHCYYSVEKDW 96  
 2 LPRTITIMSWMLLSQVQGEVARKDAPPSSRCKGSRAYGSYCALFSVKW 61

QY 97 NSSLEFCCLARDS-HLVITDQNEMSLQVLF---SEAFCWIGR-----NNSGW 142  
 Db 62 YDAMACQKRPSGHLVSLSGAEASFLSMNIKSSGNSGOYVWIGHDPTLGYPNRGGWE 122

Qy 143 WEDGSPLNFSRISN---SPVQTGAINK-NGL---QASSCEVPLHGVCX 185  
 Db 122 WSNADVMNYINWETNPSSSSGGNHCGTSLRSAGFLXWRENYCNLLFPLPVCK 171

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RESULT 9  
 CHBB\_CROHO STANDARD; PRT; 117 AA.

ID CHBB\_CROHO  
 AC P81579;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DE Pancreatitis-associated protein 3 precursor (REG III-gamma).  
 GN PAP3 OR REG3G.  
 CS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10890;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas;  
 MEDLINE=97208868; PubMed=905510;  
 RA Suzuki Y., Noguchi N., Takashawa S., Kumagai T., Miyashita H.,  
 Okamoto H.,  
 RT "structure, chromosomal localization and expression of mouse genes  
 encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";  
 RL Gene 185:159-168 (1997).  
 CC -!- FUNCTION: Might be a stress protein involved in the control of  
 CC bacterial proliferation.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Constitutively expressed in the small  
 intestine, moderately in colon and at an extremely low level in  
 healthy pancreas.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
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 or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; D63361; BAA18930; 1.  
 DR HSSP; P05451; I11T.  
 DR MGD; MG1:109406; RegIII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR InterPro; IPR003990; Pancreatitis\_ac.  
 DR Pfam; PF00059; lectin\_c; 1.

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DR PRINTS; PR01504; ENCREATITISAP.  
 DR SMART; SM00034; CUBCT; 1.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW SIGNAL; Lectin; Inflammatory response; Acute phase; Multigene family.  
 FT CHAIN 1  
 FT DOMAIN 26  
 FT DOMAIN 27 174 PANCREATITIS-ASSOCIATED PROTEIN 3.  
 FT DOMAIN 38 172 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 40 51 BY SIMILARITY.  
 FT DISULFID 68 170 BY SIMILARITY.  
 FT DISULFID 145 162 BY SIMILARITY.  
 SQ SEQUENCE 174 AA; 19307 MW; 5575E9E56A4D8CEF CRC64;

---

RESULT 9  
 CHBB\_CROHO STANDARD; PRT; 117 AA.

ID CHBB\_CROHO  
 AC P81579;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Pancreatitis-associated protein 3 precursor (REG III-gamma).  
 GN PAP3 OR REG3G.  
 CS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Crotalus.  
 OX NCBI\_TaxID=8741;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=96420502; PubMed=8823201;  
 RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,  
 RA Smith A.I., Lopez J.A., Berndt M.C.;  
 RT "Binding of a novel 50-kilodalton alboaggregin from Trimeresurus  
 RT albobatrachus and related viper venom proteins to the platelet membrane  
 RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and  
 RT glycoprotein Ib-mediated platelet activation.";  
 RL Biochemistry 35:12629-12639 (1996).  
 CC -!- FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF  
 CC binding, and stimulates agglutination.  
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC InterPro; IPR002353; AntifreezeII.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c; 1.  
 DR PRINTS; PR00354; ANTIFREEZEII.  
 DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW Lectin.  
 FT DOMAIN 9 116 C-TYPE LECTIN.  
 FT DISULFID 2 13 BY SIMILARITY.  
 FT DISULFID 30 115 BY SIMILARITY.  
 FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)  
 (POENTIAL).  
 DR Pfam; PF00059; lectin\_c; 1.

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|                    |  |           |              |                         |                                  |
|--------------------|--|-----------|--------------|-------------------------|----------------------------------|
| SQ                 | SEQUENCE   | 117 AA;   | 13888 MW;    | 07835BBCB61B9EAD CRC64; |                                  |
|                    | Query Match  | 14.3%;    | Score 146;   | DB 1;                   | Length 117;                      |
|                    | Best Local Similarity  | 28.4%;    | Prd. No. 3.  | 3.e-07;                 |                                  |
|                    | Matches  | 33;       | Conservative | 20;                     | Mismatches 57; Indels 6; Gaps 3; |
| Qy                 | 75 CPDRWMKGNHCVFSVEBDWNSLLEFOLARDSS--HIVLTIDNQENSLQVLFSEAFCW 132   |           |              |                         |                                  |
| Db                 | 2 CPDWSSEYGHCVRFQEMMTWDAEKCTQQTGHHVMSFRSEEVDLFLSKFLFW 61   |           |              |                         |                                  |
| Qy                 | 133 IGLR--NNSGWWEQDGSPLENSRISNSFVQTCGAINKNGIQAASSCEVPLHGCK 185   |           |              |                         |                                  |
| Db                 | 62 MGARDINERRLQWDGTXVNKAWSAEECIVCRATDNQWL-STCSKTHNVCK 116  |           |              |                         |                                  |
| <b>RESULT 10</b>   |  |           |              |                         |                                  |
| PAP1               | MOUSE  | STANDARD; | PRT;         | 175 AA.                 |                                  |
| ID                 | PAP1_MOUSE   |           |              |                         |                                  |
| AC                 | P35230;  |           |              |                         |                                  |
| DT                 | 01-FEB-1994 (Rel. 28, Created)   |           |              |                         |                                  |
| DT                 | 01-FEB-1994 (Rel. 28, Last sequence update)  |           |              |                         |                                  |
| DT                 | 28-FEB-2003 (Rel. 41, Last annotation update)  |           |              |                         |                                  |
| DE                 | Pancreatitis-associated protein 1 precursor (REG III-beta).  |           |              |                         |                                  |
| GN                 | PAP OR PAP1 OR REG3B.  |           |              |                         |                                  |
| OS                 | Mus musculus (Mouse).  |           |              |                         |                                  |
| OC                 | Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Futheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  |           |              |                         |                                  |
| OX                 | NCBI_TaxID=10090;  |           |              |                         |                                  |
| RN                 | [1]  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RC                 | TISSUE-Pancreas, and Small intestine;  |           |              |                         |                                  |
| RX                 | MLDBN=93176807; PubMed=7679928;  |           |              |                         |                                  |
| RA                 | Itoh T, Terakoka H, ;  |           |              |                         |                                  |
| RT                 | "Cloning and tissue-specific expression of cDNAs for the human and mouse homologues of rat pancreatitis-associated protein (PAP).";  |           |              |                         |                                  |
| RL                 | Biochim. Biophys. Acta 1172:184-186(1993).   |           |              |                         |                                  |
| RN                 | [2]  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RC                 | STRAIN-C57BL/6J; TISSUE=Pancreas; MEDLINE=97208866; PubMed=905810;   |           |              |                         |                                  |
| RX                 | Narushima Y., Unno M., Nakagawa K.-I., Mori M., Miyashita H., Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H., Okamoto H.;   |           |              |                         |                                  |
| RA                 | RT   |           |              |                         |                                  |
| RA                 | structure, chromosomal localization and expression of mouse genes encoding type III RegII alpha, RegIII beta, RegIII gamma.;   |           |              |                         |                                  |
| RA                 | Gene 185:159-168(1997).  |           |              |                         |                                  |
| RA                 | -!- FUNCTION: Might be a stress protein involved in the control of bacterial proliferation.  |           |              |                         |                                  |
| CC                 | -!- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF PANCREATIC ACINAR CELLS (BY SIMILARITY).   |           |              |                         |                                  |
| CC                 | -!- TISSUE SPECIFICITY: Constitutively expressed in the small intestine, moderately in colon and at an extremely low level in healthy pancreas.  |           |              |                         |                                  |
| CC                 | -!- INDUCTION: Appears in pancreatic juice after induction of pancreatic inflammation.   |           |              |                         |                                  |
| CC                 | -!- DISEASE: Overexpressed during the acute phase of pancreatitis.   |           |              |                         |                                  |
| CC                 | -!- SIMILARITY: Contains 1 C-type lectin family domain.  |           |              |                         |                                  |
| CC                 | -----  |           |              |                         |                                  |
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| CC                 | -----  |           |              |                         |                                  |
| DR                 | D13509, BA02727; 1;  |           |              |                         |                                  |
| DR                 | D63359; BAA18928; 1;   |           |              |                         |                                  |
| EMBL               | D63360; BAA18929; 1;   |           |              |                         |                                  |
| DR                 | PIR; S29822; S29822;   |           |              |                         |                                  |
| DR                 | HSSP; P04451; 1LIT;  |           |              |                         |                                  |
| DR                 | MDG; MGI:97478; Pap.   |           |              |                         |                                  |
| DR                 | InterPro; IPR001304; Lectin_C.   |           |              |                         |                                  |
| DR                 | InterPro; IPR003990; Pancreatis_ac.  |           |              |                         |                                  |
| DR                 | pfam; PF00059; Lectin_c_1.   |           |              |                         |                                  |
| DR                 | SMART; SM00034; CLECT_1.   |           |              |                         |                                  |
| DR                 | PROSITE; PS00615; C_TYPELECTIN_1;  |           |              |                         |                                  |
| DR                 | PROSITE; PS00041; C_TYPELECTIN_2;  |           |              |                         |                                  |
| KW                 | Signal; Lectin; Inflammatory response; Acute phase; Multigene family.  |           |              |                         |                                  |
| FT                 | SIGNAL   | 1         | 26           |                         |                                  |
| FT                 | CHAIN  | 27        | 175          |                         |                                  |
| FT                 | DOMAIN   | 38        | 173          | C-TYPE LECTIN           | 1.                               |
| FT                 | DISULFID   | 40        | 51           | BY SIMILARITY.          |                                  |
| FT                 | DISULFID   | 68        | 171          | BY SIMILARITY.          |                                  |
| FT                 | DISULFID   | 146       | 163          | BY SIMILARITY.          |                                  |
| SQ                 | SEQUENCE   | 175 AA;   | 19476 MW;    | 44B310117LE79775 CRC64; |                                  |
| <b>Query Match</b> |  |           |              |                         |                                  |
| Query              | PSGSCVIAITGLTAVILSVLQNLCOGSNNSTCASC-----SCPDRAMKYGHHCYY 88   |           |              |                         |                                  |
| Db                 | PPPTACSV-----MSWMLLSCLM-----LLSQYQGEDSLKNIPSARISCPKGQSAYGSTCYA 53  |           |              |                         |                                  |
| Qy                 | 89 FSVEERDWNSSLEFCALAR-DSHLVVTDNQENSLLQVEL-----SEAFCWIGLR-----136  |           |              |                         |                                  |
| Db                 | 54 LEQIPQWEDALACQRPGGHLVSLNSAELSSMVKRTGNSQYTWTGLHDPTLGA 113  |           |              |                         |                                  |
| Qy                 | 137 -NNSGWRWEDGSPLNSRISNSFVQT---CGA1NK-NGL---QASSCEVPLHGCK 185   |           |              |                         |                                  |
| Db                 | EPNGGGMEWSNNDDVMYFNWERNPSTALDRAFTCGSLSRASGFGLKWRDMTCERKLPTVCK 172  |           |              |                         |                                  |
| <b>RESULT 11</b>   |  |           |              |                         |                                  |
| LITH               | RAT  | STANDARD; | PRT;         | 165 AA.                 |                                  |
| ID                 | P10758;  |           |              |                         |                                  |
| AC                 | P10758;  |           |              |                         |                                  |
| DT                 | 01-JUL-1989 (Rel. 11, Created)   |           |              |                         |                                  |
| DT                 | 01-JUL-1989 (Rel. 11, Last sequence update)  |           |              |                         |                                  |
| DE                 | Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islet of langerhans regenerating protein) (ICRP).  |           |              |                         |                                  |
| DE                 | (Islet cell regeneration factor) (ICRF).   |           |              |                         |                                  |
| GN                 | REG1 OR REG.   |           |              |                         |                                  |
| OS                 | Rattus norvegicus (Rat).   |           |              |                         |                                  |
| OC                 | Batrachia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  |           |              |                         |                                  |
| OC                 | NCBI_TaxID=10116;  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RX                 | MEDLINE=91093273; PubMed=1985964;  |           |              |                         |                                  |
| RA                 | Rouquier S., Verdinier J.M., Iovanna J., Dagorn J.-C., Giorgi D.; RT   |           |              |                         |                                  |
| RA                 | "rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine cells, regulation by food content, and sequence identity with the endocrine reg transcript.";  |           |              |                         |                                  |
| RT                 | J. Biol. Chem. 263:2111-2114 (1988).   |           |              |                         |                                  |
| RL                 | J. Biol. Chem. 266:786-791 (1991).   |           |              |                         |                                  |
| RN                 | [2]  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RX                 | MBDLIN=88115343; PubMed=296300;  |           |              |                         |                                  |
| RA                 | Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y., Dusett N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L.; RT   |           |              |                         |                                  |
| RA                 | "A novel gene activated in regenerating islets.";  |           |              |                         |                                  |
| RT                 | J. Biol. Chem. 263:2111-2114 (1988).   |           |              |                         |                                  |
| RL                 | J. Biol. Chem. 266:786-791 (1991).   |           |              |                         |                                  |
| RN                 | [3]  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RX                 | MBDLIN=93326645; PubMed=7916640;   |           |              |                         |                                  |
| RA                 | Dusett N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L.; RT   |           |              |                         |                                  |
| RA                 | "Rapid PCR cloning and sequence determination of the rat lithostathine gene.";   |           |              |                         |                                  |
| RL                 | J. Biol. Chem. 263:2111-2114 (1988).   |           |              |                         |                                  |
| RN                 | [4]  |           |              |                         |                                  |
| RP                 | SEQUENCE FROM N.A.   |           |              |                         |                                  |
| RC                 | STRAN=Wispr; Dagorn J.-C., Iovanna J.L.; RT  |           |              |                         |                                  |
| RA                 | Miyashita H., Suzuki Y., Watanabe T., Unno M., Morizumi S.,  |           |              |                         |                                  |

RA Yonekura H.; Okamoto H.; "Structural and characterization of rat Reg I gene." ; RT Seikagaku 65:1082-1082(1993).  
 [5]

RN SEQUENCE OF 22-69.

RP TISSUE\_Panreas; RX MEDLINE=90031155; PubMed=2680252;

RA Adrich Z.; de Caro A.M.; Guidoni A.A.; Woudstra M.E.; Roverey M.; RT "Characterization in rat pancreatic juice of a protein homologous to the human pancreatic stone protein." ; RT Comp. Biochem. Physiol. 93B:793-797(1989).

RC -!- FUNCTION: Might act as an inhibitor of spontaneous calcium carbonate precipitation.

CC -!- TISSUE SPECIFICITY: Expressed only in regenerating islets, but not in normal pancreatic islets, insulinomas or regenerating liver.

CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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CC DR InterPro; IPR001304; Lectin\_C.

DR InterPro; IPR003990; Pancreatitis\_ac.

DR PRINTS; PF0059; lectin\_c\_1.

DR PRINTS; PR01504; PNCREATITSSAP.

DR SMART; SM00034; CLECT\_1.

DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1;

DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2;

DR PROSITE; PS50041; C\_TYPE\_LECTIN\_1;

KW Glycoprotein; Signal; Lectin.

FT SIGNAL 1 21 LITHOSTATHINE.

FT CHAIN 22 165 C-TYPE LECTIN (LONG FORM).

FT DOMAIN 33 163 BY SIMILARITY.

FT DISULFID 35 46 BY SIMILARITY.

FT DISULFID 63 161 BY SIMILARITY.

FT DISTULFID 136 153 BY SIMILARITY.

FT CARBOHYD 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 165 AA: 18672 MW: 9B61EB236B82CP8A CRC64;

Query Match 13.4%; Score 137; DB 1; Length 165;  
 Best Local Similarity 27.2%; Pred. No. 3.8e-06;  
 Matches 43; Conservative 23; Mismatches 68; Indels 24; Gaps 7;

QY 49 VLLSVLYQWLICQGSNYSCTASCP\$ ---COPDRNRYKGNHCVYFFVVEKDWNSSLFCL 104  
 DB 8 ILLSCIM---VLSPSQGEAEFDLPSARITPEGNSAYSSCTCYYFMEDHLSSWAEDLFCQ 64

QY 105 ARDS-HLLVLTIDNOENSLQYELSE ---AFCWIGH---ENNSGWRWEDOSPLNF---- 151  
 DB 65 NMNNSGIVLVSLSQAEGFLASLICKESSTAAANWIGRHHDPKNNRRWHSSGSLFLYKSWD 124

QY 152 SRISSNSFVQTGCAINKG---LQASCEVPLHGVCK 185  
 DB 125 TGYPNNNSNRGYCVSNTNSGTYKWRDNISCDQLSFVCK 162

RESULT 12

ANP\_HEMAM STANDARD; PRT; 163 AA.  
 ID ANP\_HEMAM AC P05144;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Antifreeze protein precursor (AFP).  
 OS Hemimotripterans americanus (Sea raven).  
 OC Eularyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;  
 OC Coraciidae; Hemimotripteridae; Hemimotripteridae.  
 OC NCBI\_TaxID=8094;  
 RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RX MEDLINE=87057207; PubMed=3782083;

RA NG N.F.L., Trinh K.-Y., New C.-L., Hayes P., Scott G.K., Ng N.F.L., New C.-L., Davies P.L., RT "Structure of an antifreeze polypeptide precursor from the sea raven, RT Hemimotripterans americanus." ; RT Hemimotripterans americanus." ; RT J. Biol. Chem. 261:15690-15695 (1986).  
 RL RN [2]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RX MEDLINE=90036386; PubMed=2572595;

RA Hayes P., Scott G.K., Ng N.F.L., New C.-L., Davies P.L., RT "Cystine-rich type II antifreeze protein precursor is initiated from the third AUG codon of its mRNA." ; RT J. Biol. Chem. 264:18761-18767 (1989).  
 RL RN [3]  
 RP DISULFIDE BONDS, AND SIMILARITY TO C-TYPE LECTINS.  
 RX MEDLINE=9235557; PubMed=1644794;

RA NG N.F.L., New C.-L., RT "Structure of an antifreeze polypeptide from the sea raven. Distulfide bonds and similarity to lectin-binding proteins." ; RT J. Biol. Chem. 267:16069-16075 (1992).  
 RL RN [4]  
 RP STRUCTURE BY NMR, AND REVISIONS TO DISTULFIDE BONDS.  
 RX MEDLINE=98206586; PubMed=9537986;

RA Grönwald W., Loewen M.C., Lix B., Daugulis A.J., Soennichsen F.D., Davies P.L., Sykes B.D.; RT "The solution structure of type II antifreeze protein reveals a new member of the lectin family." ; RT Biochemistry 37:4712-4721 (1998).  
 RL CC -!- FUNCTION: Antifreeze proteins lower the blood freezing point.  
 CC -!- SIMILARITY: BELONGS TO THE TYPE-II AFP FAMILY. TYPE 2 AFP ARE CYSTEINE-RICH.  
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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CC DR EMBL; J02593; AAA49617.1; ALT\_INIT.  
 DR EMBL; J05100; AAA49618.1; -.

CC DR PIR; A34313; A34313.  
 CC DR PDB; 2AEP; 23\_DEC-98.  
 CC DR InterPro; IPR02353; AntifreezeII.  
 CC DR InterPro; IPR001304; Lectin\_C.  
 CC DR Pfam; PF00059; lectin\_c\_1.  
 CC DR PRINTS; PR00356; ANTIFREEZEII.  
 CC DR SMART; SM00034; CLRECT\_1.  
 CC DR PROSITE; PS00615; C\_TYPE\_LECTIN\_1;  
 CC DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2;  
 CC KW Antifreeze protein; Lectin; Signal; 3D-structure.  
 CC FT SIGNAL 1 17 POTENTIAL.  
 CC FT PROPEP 18 34 ANTIFREEZE PROTEIN.  
 CC FT CHAIN 35 163 C-TYPE LECTIN (LONG FORM) .

CC DR DOMAIN 39 163  
 CC FT DISULFID 41 52  
 CC FT DISULFID 69 159  
 CC FT DISULFID 103 134  
 CC FT DISULFID 123 145  
 CC FT CONFLICT 135 151  
 CC FT STRAND 52 53  
 CC FT HELIX 62 72

|                       |   |
|-----------------------|---|
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| CC                    | DR  |
| CC                    | EMBL; M39794; AAA30750.1; -   |
| CC                    | DR  |
| FT                    | PIR; A37194; A37194.  |
| FT                    | HSSP; P05451; 1QDD.   |
| FT                    | InterPro; IP001304; Lectin_C.   |
| FT                    | InterPro; IPR003990; Pancreatitis_ac.   |
| FT                    | PFam; PF00559; Lectin_C_1.  |
| FT                    | PRINTS; PRO1504; PNCREATINITSAP.  |
| FT                    | SMART; SM0034; CLectC_1.  |
| FT                    | PROSITE; PS00615; C_TYPELECTIN_1;   |
| FT                    | PROSITE; PS50041; C_TYPELECTIN_2;   |
| FT                    | KW Glycoprotein; Signal; Lectin.  |
| FT                    | SIGNAL 1 26 POTENTIAL.  |
| FT                    | FT PROPEP 27 37 POTENTIAL.  |
| FT                    | FT CHAIN 38 175 LIPTOSTATINE.   |
| FT                    | FT CHAIN 38 138 A CHAIN.  |
| FT                    | FT CHAIN 141 175 B CHAIN.   |
| FT                    | FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM) .  |
| FT                    | FT DISULFID 40 51 BY SIMILARITY.  |
| FT                    | FT DISULFID 68 171 BY SIMILARITY.   |
| FT                    | FT DISULFID 146 163 BY SIMILARITY.  |
| FT                    | FT CONFLICT 84 85 BE > FF (IN REF. 3).  |
| SQ                    | SEQUENCE 175 AA; 19334 MW; C2700E70B7E91D6A CRC64;  |
| Query Match           | Score 13.1%; Score 134.5%; DB 1; Length 175;  |
| Best Local Similarity | 27.4%; Pred. No. 7.1e-06;   |
| Matches               | 26; Conservative 10; Mismatches 42; Indels 4; Gaps 2;   |
| QY                    | 73 PSCPDWMMKGNHCKYYESVERKDWNSSLEFFCLARDSHLIVITDNQEMSLLOVFLSERFCW 132  |
| QY                    | :    :    :    :    :    :    :    :    :    :  |
| Db                    | 39 BNCPAGHQPLGRCIVYTATTAMTWAAETNCMKGHLASTHSQEEHSFIQT-LNAGVWW 97   |
| QY                    | 133 IG---LRNNSGRWRWEDSPLNF 151  |
| Db                    | 98 IGGSAQIQAQAWTWSQDTTPMF 119   |
| RESULT 13             | LITH_BOVIN STANDARD; PRT; 175 AA.   |
| RP                    | SEQUENCE FROM N.A. MEDLINE=90368981; PubMed=2394826;  |
| RX                    | de la Monte S.M.; Ozturk M.; Wands J.R.; RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease and the developing human brain." ;  |
| RL                    | J. Clin. Invest. 86:1004-1013 (1990). [2]   |
| RN                    | SEQUENCE OF 38-138 AND 141-175.   |
| RX                    | MEDLINE=91197389; PubMed=1085387;   |
| RA                    | Cai L.; Harris W.R.; Marshak D.R.; Gross J.; Crabb J.W.; DE "Structural analysis of bovine pancreatic thread protein." ;  |
| RA                    | J. Protein Chem. 9:623-632 (1990). [3]  |
| RN                    | SEQUENCE OF 38-85 AND 141-175.  |
| RX                    | Gross J.; Brauer A.W.; Bringhurst R.F.; Corbett C.; Margolies M.N.; RT "An unusual bovine pancreatic protein exhibiting pH-dependent globule-fibril transformation and unique amino acid sequence." ;   |
| RL                    | Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631 (1985). [4]  |
| CC                    | -!- FUNCTION: Might act as an inhibitor of spontaneous calcium carbonate precipitation.   |
| CC                    | -!- SUBUNIT: Cleaved to give an A chain and a B chain joined by a disulfide bond.   |
| CC                    | -!- TISSUE SPECIFICITY: In pancreatic acinar cells.   |
| CC                    | -!- SIMILARITY: Contains 1 C-type lectin family domain.   |
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| CC                    | SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas; RT 005037; AC 005037; DT 01-NOV-1997 (Ref. 35, Created); DT 01-NOV-1997 (Ref. 35, Last sequence update)   |
| CC                    | DE Pancreatitis-associated protein 2 precursor (Lithostathine 3) (Islet of Langerhans regenerating protein 3) (REG 3) (REG III alpha). DE PAP2 OR REG3A. OS Mus musculus (Mouse).   |
| CC                    | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buterophila; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=100900; OX  |
| RN                    | SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Liver, and Pancreas; RT 005037; AC 005037; DT 01-NOV-1997 (Ref. 35, Created); DT 01-NOV-1997 (Ref. 41, Last annotation update)   |
| CC                    | RA Narushima Y.; Unno M.; Nakagawa K.-I.; Mori M.; Miyashita H.; Suzuki Y.; Noguchi N.; Takasawa S.; Kumagai T.; Yonekura H.; Okamoto H.; RT encoding type I1 Reg; REGIII alpha, REGIII beta, REGIII gamma.; CC bacterial proliferation. CC -!- FUNCTION: Might be a stress protein involved in the control of small intestine and pancreas.  |
| CC                    | -!- TISSUE SPECIFICITY: Small intestine and pancreas.   |
| CC                    | -!- SUBCELLULAR LOCATION: Secreted.   |
| CC                    | CC "Structure, chromosomal localization and expression of mouse genes Gene 185:159-168 (1997)."   |
| CC                    | CC -!- FUNCTION: Might be a stress protein involved in the control of   |
| CC                    | CC bacterial proliferation.   |
| CC                    | CC -!- TISSUE SPECIFICITY: Small intestine and pancreas.  |
| CC                    | CC -!- SUBCELLULAR LOCATION: Secreted.  |

```

CC is inhibited.
CC -1- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
CC linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
CC RANGE=24-146
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC
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CC
CC DR EMBL; AB019616; BAA34425.1; -
CC DR HSSP; P23807; 1IIX.
CC DR GO; GO:0005516; C:extracellular; IC.
CC DR GO; GO:0007596; P:blood coagulation; IDA.
CC DR InterPro; IPR01304; Lectin_C.
CC DR Pfam; PF00059; Lectin_c; 1.
CC DR SMART; SM00034; CLECT; 1.
CC DR PROSITE; PS00615; C_TYPELECTIN_1; 1.
CC DR PROSITE; PS0041; C_TYPELECTIN_2; 1.
CC KW Blood coagulation; Lectin; Signal.
CC FT SIGNAL 1 23
CC CHAIN 1 24 MAMUSHIGIN BETA CHAIN.
CC FT DOMAIN 1 32 146
CC FT DOMAIN 1 32 143 C-TYPE LECTIN.
CC FT DISULFID 1 36 BY SIMILARITY.
CC FT DISULFID 1 53 142 BY SIMILARITY.
CC FT DISULFID 1 98 98 INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
CC FT DISULFID 1 119 134 (BY SIMILARITY).
CC SQ SEQUENCE 146 AA; 17064 MW; 9EDAB4BDCC24E76D CRC64;

Query Match 13.1%; Score 134; DB 1; Length 146;
Best Local Similarity 28.6%; Pred. No. 6.5e-06;
Matches 36; Conservative 18; Mismatches 50; Index 22; Gaps 6;
Query 75 CPDRWWKYGHNCHCYFFSYKEWDQNSSEFLCL--ARDSHLLVITDNEQ---MSLLQYFLSE 128
Db 25 CPDWSSTSEGHCVRFQEMMTWDAEKFTQORKSHLSVSFSSEYDFVIVSMTWPLKY 84
Query 129 AFOWIGLRLNNSGW----RWEDGSPLNFSRISNSFYQTGAI----NKNGHQASSCEVP 179
Db 85 DFWIGL--NNIWNCKMVENTDG----TRLSHNAITESECTAAKITTDNOWLSPCSRT 137
Query 180 LHGVCK 185
Db 138 YNVVCK 143

Search completed: August 10, 2004, 16:34:04
Job time : 14 secs

```

| SUMMARIES  |       |       |        |        |        |                          |
|------------|-------|-------|--------|--------|--------|--------------------------|
|            | %     | Query | Match  | Length | ID     | Description              |
| result No. | Score | Match | Length | DB     | ID     |                          |
| 1          | 1023  | 100.0 | 189    | 4      | 043198 | 043118 homo sapien       |
| 2          | 1007  | 98.4  | 189    | 4      | 075613 | 075613 homo sapien       |
| 3          | 548.5 | 53.6  | 188    | 11     | 089713 | 089713 mus musculus      |
| 4          | 525.5 | 51.4  | 188    | 11     | Q64335 | Q64335 rattus norvegicus |
| 5          | 194.5 | 22.0  | 181    | 4      | Q9NZS1 | Q9NZS1 homo sapien       |
| 6          | 189.5 | 19.0  | 178    | 11     | Q912W9 | Q912W9 mus musculus      |
| 7          | 189.5 | 18.5  | 179    | 6      | QBMJ13 | QBMJ13 pongo pygmaeus    |
| 8          | 189.5 | 18.5  | 179    | 6      | QBMHY8 | QBMHY8 pongo pygmaeus    |
| 9          | 189.5 | 18.3  | 179    | 11     | Q35778 | Q35778 rattus norvegicus |
| 10         | 186.5 | 18.2  | 179    | 6      | QBMHY9 | Q8mbhy9 pongo pygmaeus   |
| 11         | 186.5 | 18.2  | 179    | 6      | QBMJ14 | Q8mbj14 pongo pygmaeus   |
| 12         | 186.5 | 18.1  | 132    | 11     | Q8R4K5 | Q8r4k5 rattus norvegicus |
| 13         | 185   | 18.1  | 163    | 6      | Q9GK90 | Q9gk90 macaca mulatta    |
| 14         | 184.5 | 18.0  | 159    | 6      | Q8SPX0 | Q8spx0 sus scrofa        |
| 15         | 184.5 | 18.0  | 183    | 13     | Q54708 | Q54708 gallus gallus     |
| 16         | 183.5 | 17.9  | 179    | 11     | Q54708 | Q54708 mus musculus      |

|    |     |   |                       |  |   |         |
|----|-----|---|-----------------------|--|---|---------|
| Db | 1   | MDSVIVSMLLEPTATAQNDYGPQQKSSSSPKPSCSLVAVTGLITAVLISVLVQWIL 60       | 088713                | PRELIMINARY;   | PRT;  | 188 AA. |
| Qy | 61  | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    | AC                    | 088713;  |   |         |
| Db | 61  | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    | DT                    | 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  |   |         |
| Qy | 121 | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 | DT                    | 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  |   |         |
| Db | 121 | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 | DE                    | Mast cell function-associated antigen 2F1 (MFA) (Killer cell lectin-like receptor G1).   |   |         |
| Qy | 181 | HGVCKKVRLL 189  | DE                    | GN   | KLRG1 OR MFA  |         |
| Db | 181 | HGVCKKVRLL 189  | OS                    | Mus musculus (Mouse).  |   |         |
| Qy |     |   | OC                    | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.                  |   |         |
| Db |     |   | OC                    | NCBI_TaxID=10030;  |   |         |
|    |     |   | RN                    | [1]  |   |         |
|    |     |   | RP                    | SEQUENCE FROM N.A.   |   |         |
|    |     |   | RC                    | STRAIN=C.B17 SCID;   |   |         |
|    |     |   | RX                    | Medline=93071514; PubMed=9862378;  |   |         |
|    |     |   | RA                    | Hanke T.; Corral L.; Vance R. E.; Raulet D.H. i.   |   |         |
|    |     |   | RT                    | "2F1 antigen, the mouse homolog of the rat 'SI', is a lectin-like type II transmembrane receptor expressed by natural killer cells."                 |   |         |
|    |     |   | RL                    | Eur. J. Immunol. 28:4409-4417(1998).   |   |         |
|    |     |   | RN                    | [2]  |   |         |
|    |     |   | RP                    | SEQUENCE OF 2-188 FROM N.A.  |   |         |
|    |     |   | RA                    | Blaser C. i.   |   |         |
|    |     |   | RL                    | Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.   |   |         |
|    |     |   | RN                    | [3]  |   |         |
|    |     |   | RP                    | SEQUENCE FROM N.A.   |   |         |
|    |     |   | RC                    | STRAIN=129/SvEvTacFBr; TISSUE-Spleen;  |   |         |
|    |     |   | RX                    | Medline=21115136; PubMed=11221622;   |   |         |
|    |     |   | RA                    | Voehringer D.; Kaufmann M.; Pircher H. i.  |   |         |
|    |     |   | RT                    | "Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor GI gene (KLRGI), the mouse homologue of MFA." |   |         |
|    |     |   | RL                    | ImmunoGenetics 52:206-211(2001).   |   |         |
|    |     |   | DR                    | EMBL; AF091357; AAD03181.1;  |   |         |
|    |     |   | DR                    | EMBL; AJ010751; CAA09342.1;  |   |         |
|    |     |   | DR                    | EMBL; AF317727; AAKA0082.1;  |   |         |
|    |     |   | DR                    | MGD; MGJ:13515294; KLRGI.  |   |         |
|    |     |   | DR                    | GO:0004872; F:sugar binding; IEA.  |   |         |
|    |     |   | DR                    | GO:0005529; F:sugar binding; IEA.  |   |         |
|    |     |   | DR                    | GO:0000157; P:heparophilic cell adhesion; IEA.   |   |         |
|    |     |   | DR                    | InterPro; IPR001304; Lectin_C.   |   |         |
|    |     |   | DR                    | Pfam; PF00059; lectin_c_1.   |   |         |
|    |     |   | DR                    | SMART; SM00034; CLBCT;   |   |         |
|    |     |   | DR                    | PROSITE; PS50041; C_TYPELECTIN_2_1.  |   |         |
|    |     |   | KW                    | Lectin_Receptor.   |   |         |
|    |     |   | SQ                    | SEQUENCE 188 AA; 21396 MW; 876336802EA134F1 CRC64;   |   |         |
|    |     |   | Query Match           | 53.6%; Score 548.5;  |   |         |
|    |     |   | Best Local Similarity | 55.6%;   |   |         |
|    |     |   | Matches 104;          | Score 548.5;   |   |         |
|    |     |   | Conservative          | DB 11;   |   |         |
|    |     |   | 1                     | Length 188;  |   |         |
|    |     |   | 1                     | Indels 56;   |   |         |
|    |     |   | 1                     | Gaps 1;  |   |         |
| Qy | 1   | MDSVIVSMLLEPTATAQNDYGPQQKSSSSPKPSCSLVAVTGLITAVLISVLVQWIL 60       | Qy                    | 1  | MDSVIVSMLLEPTATAQNDYGPQQKSSSSPKPSCSLVAVTGLITAVLISVLVQWIL 60       |         |
| Db | 1   | MDSVIVSMLLEPTATAQNDYGPQQKSSSSPKPSCSLVAVTGLITAVLISVLVQWIL 60       | Db                    | 1  | MDSVIVSMLLEPTATAQNDYGPQQKSSSSPKPSCSLVAVTGLITAVLISVLVQWIL 60       |         |
| Qy | 61  | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    | Qy                    | 61   | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    |         |
| Db | 61  | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    | Db                    | 61   | CQGSNYSTCASCSPCPDRWMKYGNHCYFSVEKDNNNLSLEFCLARDSHLLVITDQEMS 120    |         |
| Qy | 121 | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 | Qy                    | 121  | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 |         |
| Db | 121 | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 | Db                    | 121  | LLOQVELSEAFCWIGLIPNNSGWRWEDGSPLNFSRISNSFVOTCGAINKNGIQAASSCVPL 180 |         |
| Qy | 181 | HGVCKKVRLL 189  | Qy                    | 181  | HGVCKKVRLL 189  |         |
| Db | 181 | HGVCKKVRLL 189  | Db                    | 181  | HGVCKKVRLL 189  |         |
|    |     |   | RESULT 4              |  |   |         |
|    |     |   | Q64335                |  |   |         |
|    |     |   | ID Q64335             |  |   |         |
|    |     |   | AC Q64335;            |  |   |         |
|    |     |   | RESULT 3              |  |   |         |

|            |  |    |   |
|------------|--|----|---|
| DT         | 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  | RA | "Human KLRF1, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis."; |
| DT         | 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  | RT | RT  |
| DE         | MAFA protein.  | RT | RT  |
| GN         | MAFA.  | RT | RT  |
| OS         | Batrachospermum norvegicum (Rat).  | RL | mapping to the NK gene complex and expression analysis.";   |
| OC         | Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  | DR | Eur. J. Immunol. 30:168-176 (2000).   |
| NCBI_TAXID | Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.   | DR | EMBL; AF115207; AF378051; -.  |
| [1]        | Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.   | DR | GO; GO:0016020; C:membrane; TAS.  |
| RN         | SEQUENCE FROM N.A. STRAIN=SPRAUKE DAWLEY; TISSUE=Testis; Boeve Jr P., Gutmann M.D., Pecht I.; [2]  | DR | GO; GO:0030106; F:MHC class I receptor activity; TAS.   |
| RP         | SEQUENCE FROM N.A. MEDLINE=96016176; PubMed=7568140; Guttman M.D., Tal M., Pecht I.; A secretion inhibitory signal transduction molecule on mast cells is another C-type lectin."; Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995). | DR | InterPro; IPR01304; Lectin_C.   |
| RN         | SEQUENCE FROM N.A. RT  | DR | Pfam; PF00059; Lectin_c_1.  |
| RX         | RT   | DR | SMART; SM00034; CLECT1.   |
| RA         | RT   | DR | PROSITE; PS50041; C_TYPE_LECTIN_2; 1.   |
| RL         | RT   | DR | Receptor.   |
| RN         | SEQUENCE FROM N.A. RT  | DR | KW  |
| RX         | RT   | DR | SEQUENCE 181 AA; 21204 MW: 64642240CAE1E551 CRC64;  |
| RA         | RT   | DR | Query Match 22.0%; Score 225; DB 4; Length 181;   |
| RL         | RT   | DR | Best Local Similarity 33.6%; Pred. No. 1..1e-16;  |
| RN         | SEQUENCE FROM N.A. RT  | DR | Matches 51; Conservative 26; Mismatches 45; Indels 30; Gaps 6; SEQENCE 181 AA.  |
| RX         | RT   | DR | Qy 44 GLLTAVILSVLVYQWLQGNSNYSTACPSCPSCDRAWMKGNHCCYFSVEEKDNNSLEPC 103  |
| RA         | RT   | DR | 49 GLLTAVILSVLVYQWLQGNSNYSTACPSCPSCDRAWMKGNHCCYFSVEEKDNNSLEPC 92  |
| RL         | RT   | DR | Qy 104 LARDSHLIVITDQNEMGLQVLESEA -FCWIGERNNS --GMRWEDGSPLNFNSRISNSF 159   |
| RN         | SEQUENCE FROM N.A. RT  | DR | 93 LERKSHLIITDQNEMGLQVLESEA -FCWIGERNNS --GMRWEDGSPLNFNSRISNSF 148  |
| RX         | RT   | DR | Qy 160 VQ-----TGAIAINKNLQASSEEVPLHGKVCK 185   |
| RA         | RT   | DR | Qy 149 IKGPAAKENSCKAIEKSKFESERCSSSVFKWICQ 180   |
| RL         | RT   | DR | RESULT 6 Q91ZM9   |
| RN         | SEQUENCE FROM N.A. RT  | DR | ID Q91ZM9 PRELIMINARY; PRT; 178 AA.   |
| RX         | RT   | DR | AC Q91ZM9_  |
| RA         | RT   | DR | DT 01-DEC-2001 (TRIMBLrel. 19, Created)   |
| RL         | RT   | DR | DT 01-DEC-2001 (TRIMBLrel. 19, Last sequence update)  |
| RN         | SEQUENCE FROM N.A. RT  | DR | DT 01-DEC-2003 (TRIMBLrel. 25, Last annotation update)  |
| RX         | RT   | DR | DB SIGNR2.  |
| RA         | RT   | DR | GN CD2039 OR SIGNR2.  |
| RL         | RT   | DR | MS musculus (Mouse)   |
| RN         | SEQUENCE FROM N.A. RT  | DR | OS Buxarayota; Metarcoa; Chordata; Craniata; Vertebrata; Buteleostomi;  |
| RX         | RT   | DR | OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.   |
| RA         | RT   | DR | NCBI_TAXID=10090; OX  |
| RL         | RT   | DR | RN "Five mouse homologues of the human dendritic cell C-type lectin, DC-SIGN.",   |
| RN         | SEQUENCE FROM N.A. RT  | DR | RP STRAIN=C57BL/6;  |
| RX         | RT   | DR | PubMed=11581173;  |
| RA         | RT   | DR | RA Park C.G., Takakura K., Umemoto E., Yashima Y., Matsubara K.,  |
| RL         | RT   | DR | RA Matsuda Y., Clausen B.E., Inaba K., Steiman R.M.; Murinae; Murinae; Mus.   |
| RN         | SEQUENCE FROM N.A. RT  | DR | RT "Five mouse homologues of the human dendritic cell C-type lectin, DC-SIGN.",   |
| RX         | RT   | DR | RL Int. Immunol. 13:1283-1290 (2001).   |
| RA         | RT   | DR | DR EMBL; AF373410; AAL13236; 1; -.  |
| RL         | RT   | DR | DR MGD; MGI: 2157945; Cdd09c.   |
| RN         | SEQUENCE FROM N.A. RT  | DR | DR GO; GO:0005529; F:sugar binding; IEA.  |
| RX         | RT   | DR | DR InterPro; IPR02353; AntifreezeII.  |
| RA         | RT   | DR | DR InterPro; IPR01304; Lectin_C.  |
| RL         | RT   | DR | DR Pfam; PF00059; Lectin_c_1.   |
| RN         | SEQUENCE FROM N.A. RT  | DR | DR Prints; PR00356; AntifreezeII.   |
| RX         | RT   | DR | DR SMART; SM00034; CLECT1.  |
| RA         | RT   | DR | DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.  |
| RL         | RT   | DR | DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.  |
| RN         | SEQUENCE FROM N.A. RT  | DR | SEQUENCE 178 AA; 21245 MW: 034F9ACE02BD9032 CRC64;  |
| RX         | RT   | DR | Query Match 19.0%; Score 194.5; DB 11; Length 178;  |
| RA         | RT   | DR | Best Local Similarity 31.0%; Pred. No. 2..6e-13;  |
| RL         | RT   | DR | Matches 39; Conservative 23; Mismatches 53; Indels 11; Gaps 3;  |
| RN         | SEQUENCE FROM N.A. RT  | DR | Qy 72 CPSCPDRMKYGNHCCYFSVEEKDNNSLEPCFLARDSLVITINQEMSLLQVLF-EF 130   |
| RX         | RT   | DR | 45 CRCPWPWDTVFGCNCYFSKEQWNWDSVNAACKRLDAQUVLKSDFQQTSEKGY 104   |

RESULT 7  
 QY 131 CWIG--LRNNSGWRVEDGSPLNFSR|S-----SNSFVOTCGAINKNGQASSCCEVPL 180  
 DR 105 AWGMGLSLKHEGRWHTVGSHLFLPSMKYWKGPENNEWEDCAEFRGDWNDAFTIKK 164  
 QY 181 HGVCKK 186  
 DR 165 YWICKK 170

SEQUENCE FROM N.A.  
 ID Q8MUT3 PRELIMINARY; PRT; 179 AA.  
 AC DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 AC DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DR Natural killer cell receptor.  
 GN POPY-CD94.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Pongo.  
 RN NCBI\_TAXID=9600;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22072192; PubMed=12077248;  
 RA Guethlein L.A.; Flodin L.R.; Adams E.J.; Parham P.;  
 RT "NK Cell Receptors of the Orangutan (Pongo Pygmaeus): A Pivotal  
 Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors  
 with MHC-C.";  
 RT J. Immunol. 169:220-229 (2002).  
 DR EMBL: AF470381; AAC78481.1; -.  
 DR EMBL: AF470382; AM78482.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c\_1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 KW Receptor.  
 SQ SEQUENCE 179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;

Query Match 18.5%; Score 189 5; DB 6; Length 179;  
 Best Local Similarity 28.6%; Pred. No. 9.4e-13;  
 Matches 50; Conservative 29; Mismatches 61; Indels 35; Gaps 7;

QY 38 IVAITIGLTLAVILSYLIVOMILCQGS-----NYSTCACPSCPDRWMK 81  
 DR 11 LISGIGIIICISLMLATL--GILLKNSFTLISIEPAFTCPDPDIELQKDSNCSCOEKWVG 67  
 QY 82 YGNHCCYFSVBEKDWNSSLEFLCLARDSHLIVITDQEMSLIQVFLSEAFCWIGL--RNN 138  
 DR 68 YRCNCYFISSEQKTNESRHLCASOKSSLQLQNTDELDFMS--SSQQFWIGLYSYEEH 125  
 QY 139 SGMRWEDGSPLN-----FERRISNSFSVQTOGAKNG-LQASSCEVPLHGVCKK 186  
 DR :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 DR 126 TAWLWENGSSLSQYLFPLFETNP---KNCIAYNPNGNALDESCDKRYICKQ 176

RESULT 9  
 ID 035778 PRELIMINARY; PRT; 179 AA.  
 AC 035778; PRT; 179 AA.  
 DR SEQUENCE FROM N.A.  
 AC 035778;  
 DR 01-JAN-1998 (TREMBLrel. 05, Created)  
 DR 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DR 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 GN CD94.  
 OS Rattus norvegicus (Rat).  
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1] RSEQUENCE FROM N.A.  
 RC STRAIN=F44;  
 RX MEDLINE=27431992; PubMed=9295048;  
 RA Dissen E.; Berg S.F.; Westgaard I.H., Possum S.;  
 RT "Molecular characterization of a gene in the rat homologous to human  
 RT CD94.";  
 RL Eur. J. Immunol. 27:2080-2086(1997).  
 DR EMBL: AF009133; AAC1022.1; -.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001304; Lectin\_C.  
 DR Pfam; PF00059; lectin\_c\_1.  
 DR SMART; SM00034; CLECT\_1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 SQ SEQUENCE 179 AA; 20781 MW;

Query Match 18.3%; Score 187; DB 11; Length 179;  
 Best Local Similarity 31.1%; Pred. No. 1.8e-12;  
 Matches 41; Conservative 25; Mismatches 50; Indels 16; Gaps 5;

RESULT 8  
 QY 131 CWIG--LRNNSGWRVEDGSPLNFSR|S-----SNSFVOTCGAINKNGQASSCCEVPL 180  
 DR 105 AWGMGLSLKHEGRWHTVGSHLFLPSMKYWKGPENNEWEDCAEFRGDWNDAFTIKK 164  
 QY 181 HGVCKK 186  
 DR 165 YWICKK 170

SEQUENCE FROM N.A.  
 ID Q8MUT3 PRELIMINARY; PRT; 179 AA.  
 AC DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
 AC DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DR Natural killer cell receptor.  
 GN POPY-CD94.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarhini; Hominidae; Pongo.  
 RN NCBI\_TAXID=9600;





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Search completed: August 10, 2004, 16:34:58  
Job time : 43 secs

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XX This is the amino acid sequence of human mast cell function-associated antigen (MAFA), a type II membrane glycoprotein, cDNA (see AAW84198) encoding human MAFA can be obtained from myelogenous leukaemic cell line KU812 or cDNA derived from human lung tissue. The encoded protein is similar to the rat form (see AAW88277) having an intracellular domain containing a putative immunoreceptor tyrosine activation motif (ITIM) and an extracellular lectin-like domain. 2 Alternative spliced forms (see AAW88266-67) of human MAFA have been identified. Polypeptides and synthetic peptides (see AAW88258-64) based on these truncated MAFA proteins can be used in methods for the treatment of inflammatory and allergic diseases, and tumour growth.

XX Sequence 189 AA;

Query Match 100.0%; Score 1023; DB 2; Length 189;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98; Mismatches 0; Indels 0; Gaps 0;  
Matches 189; Conservative 0; Score 1023; DB 4; Length 189;  
SQ Sequence 189 AA;

```

QY 1 MTDSVITYSMELPLPTAQNDYGPQQKSSSKPSCSCLVAITGLITAVLLSVLYQWIL 60
Db 1 MTDSVITYSMELPLPTAQNDYGPQQKSSSKPSCSCLVAITGLITAVLLSVLYQWIL 60
Db 61 CQGSNYSCTACSCPSCPDRMKYGNHCYFVEEKDNNSLLEFCIARDSHLLVTDNQEMS 120
Db 61 CQGSNYSCTACSCPSCPDRMKYGNHCYFVEEKDNNSLLEFCIARDSHLLVTDNQEMS 120
QY 121 LLQVFELSEAFCWIGLRNNSWRWEDSPINFSRISNSFYQTGAINKNGLQASSCEVPL 180
Db 121 LLQVFELSEAFCWIGLRNNSWRWEDSPINFSRISNSFYQTGAINKNGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

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RESULT 2  
AAE11759 standard; protein; 189 AA.

XX Human; pharmaceutical composition; mast cell function associated antigen; KW MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; KW immunosuppressive; cytostatic.

DB Human mast cell function associated antigen (MAFA) protein.  
XX Homo sapiens.  
XX WO200170805-A2.  
XX 27-SSBP-2001.  
XX 16-MAR-2001; 2001WO-US008596.  
XX Takahashi N, Mikayama T;  
XX PR WPI; 2001-611482/70.  
XX DR N-P5DBB; AAD18734.

XX Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

XX Claim 10; Page 18; 49PP; English.

CC The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is human MAFA protein.

XX CC Query Match 100.0%; Score 1023; DB 4; Length 189;  
Best Local Similarity 100.0%; Pred. No. 1.8e-98; Mismatches 0; Indels 0; Gaps 0;  
Matches 189; Conservative 0; Score 1023; DB 4; Length 189;  
SQ Sequence 189 AA;

```

QY 1 MTDSVITYSMELPLPTAQNDYGPQQKSSSKPSCSCLVAITGLITAVLLSVLYQWIL 60
Db 1 MTDSVITYSMELPLPTAQNDYGPQQKSSSKPSCSCLVAITGLITAVLLSVLYQWIL 60
Db 61 CQGSNYSCTACSCPSCPDRMKYGNHCYFVEEKDNNSLLEFCIARDSHLLVTDNQEMS 120
Db 61 CQGSNYSCTACSCPSCPDRMKYGNHCYFVEEKDNNSLLEFCIARDSHLLVTDNQEMS 120
QY 121 LLQVFELSEAFCWIGLRNNSWRWEDSPINFSRISNSFYQTGAINKNGLQASSCEVPL 180
Db 121 LLQVFELSEAFCWIGLRNNSWRWEDSPINFSRISNSFYQTGAINKNGLQASSCEVPL 180
QY 181 HGVCCKVRL 189
Db 181 HGVCCKVRL 189

```

RESULT 3  
ADD25635 standard; protein; 189 AA.

XX AC ADD25635;  
XX AC ADD25635;  
XX DT 15-JAN-2004 (first entry)  
XX Binding domain-immunoglobulin fusion protein-associated protein #95.  
DB Binding domain; immunoglobulin; fusion protein; cytostatic;  
KW antiarthritic; immunosuppressive; antidiabetic; antihyroid;  
KW neuroprotective; hinge region; immunoglobulin heavy chain;  
KW CH2 constant region; CH3 constant region; IgG1;  
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;  
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.  
XX Unidentified.  
OS OS  
XX PN US20031118592-A1.  
XX PD 26-JUN-2003.  
XX PF 25-JUL-2002; 2002US-00207655.  
XX PR 17-JAN-2001; 2001US-0367358P.  
PR 17-JAN-2002; 2002US-00093530.  
PR 03-JUN-2002; 2002US-0386691P.  
PA (GENE-) GENECRAFT INC.  
XX PA  
XX PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;



Db 121 LFGEVYLQDIFYWIGLRLNIDGWRWEGGPALSL-RILTNLSLIQRGCAIHRNGLQASSCEVAL 179  
 QY 181 HGVCKKV 187  
 :|||  
 Db 180 QWICKKV 186

RESULT 5  
 AAR7033 ID AAR7033 standard; protein; 188 AA.  
 XX  
 Mast cell function-associated antigen; MAFa; soluble; ligand;  
 identification; screening; inflammation; allergic; prevention.  
 XX  
 01-FEB-1996 (first entry)  
 XX  
 DB Mammalian mast cell function-associated antigen (MAFa).  
 XX  
 Mast cell function-associated antigen; MAFa; soluble; ligand;  
 identification; screening; inflammation; allergic; prevention.  
 XX  
 OS Rattus rattus.  
 XX  
 WO9527734-A1.  
 XX  
 19-OCT-1995.  
 XX  
 PF 06-APR-1995; 9SWO-US004258.  
 XX  
 PR 08-APR-1994; 94IL-00109257.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (RYCUT/) RYCUS A.  
 XX  
 PI Pecht I, Guthmann MD, Tal M;  
 XX  
 DR WPI: 1995-366356/47.  
 DR N-PSDB; AAT01471.  
 XX  
 Novel DNA encoding a mast cell function-associated antigen (MAFa) - useful for screening for ligands of MAFa which are useful for prevention of inflammatory and allergic reactions.  
 XX  
 PS Claim 12; Page 37; 54pp; English.  
 XX  
 A soluble form of mast cell function-associated antigen (MAFa) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFa to prevent inflammatory and allergic reactions Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;  
 Best Local Similarity 53.5%; Pred. No. 1.7e-46;  
 Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  
 Seq 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60  
 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60

QY 1 MTDIVTYSMELPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60  
 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60

Db 61 CGGSNYSTCASCSPCPDRWWKGNHCCYFSYEEDWNNSLEFCLARDSHLVLITQNQEMS 120  
 61 CGGSKGEMCSQSRCPNLMRNGSHCYFSMEKRDNSSLFCADKGSHLTLFPDNQGVN 120

Db 61 CGGSKGEMCSQSRCPNLMRNGSHCYFSMEKRDNSSLFCADKGSHLTLFPDNQGVN 120

QY 121 LLQVFELSEAFCWIGLRLNNSGWRWEDGSPLNFSRISSNSFYQTQCGAINKNGLQASSCEVPL 180  
 121 LFQEYXGDFTWIGLRDIDGRWEDGPALSLS-ILSNNSVYQKCGTTHRCGLHASSCEVAL 179

Db 121 LLQVFELSEAFCWIGLRLNNSGWRWEDGSPLNFSRISSNSFYQTQCGAINKNGLQASSCEVPL 180  
 121 LFQEYXGDFTWIGLRDIDGRWEDGPALSLS-ILSNNSVYQKCGTTHRCGLHASSCEVAL 179

QY 181 HGVCKKV 187  
 :|||  
 Db 180 QWICKKV 186

RESULT 6  
 AAW8277 ID AAW8277 standard; protein; 188 AA.  
 XX  
 AC AAW8277;  
 XX  
 DT 29-MAR-1999 (first entry)  
 XX  
 DE Rat mast cell function-associated antigen (MAFa).  
 XX  
 Mast cell function-associated antigen; MAFa; splice variant; rat;  
 inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 82 .84  
 /note= "Asn is N-glycosylated"  
 FT Modified-site 97 .99  
 /note= "Asn is N-glycosylated"  
 XX  
 PN WO954209-A2.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PP 29-MAY-1998; 98WO-GB001572.  
 XX  
 PR 31-MAY-1997; 97GB-00011148.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PJ Hewitt EL, Lamers MBA,C, Lamont A, Williams DH;  
 XX  
 DR WPI: 1999-059006/05.  
 DR N-PSDB; AAV84222.  
 XX  
 New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  
 PT Disclosure; Fig 4; 44pp; English.  
 PS This is the amino acid sequence of rat mast cell function-associated CC antigen (MAFa), a type II membrane glycoprotein found on mast cells and CC basophils. The invention relates to cloning of the human MAFa molecule CC (see AAW8275) and to the discovery of splice variants (see AAW8266-67) CC of human MAFa that are not found in rat. Polypeptides and synthetic CC peptides (see AAW8258-64) based on human MAFa and human truncated MAFa, CC and polymucleotides encoding them, can be used in methods for the CC treatment of inflammatory and allergic diseases (e.g. rheumatoid CC arthritis and asthma), and tumour growth.  
 XX  
 SQ Sequence 188 AA;

Query Match 51.4%; Score 525.5; DB 2; Length 188;  
 Best Local Similarity 53.5%; Pred. No. 1.7e-46;  
 Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  
 Seq 1 MTDSIVTYSMELPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60  
 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60

QY 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60  
 1 MADNSIYSTLEPLPTAQDNQDGPQQRSSSSXPSCCLVAVITGLITAVLLSLLVQWIL 60

Db 61 CGGSNYSTCASCSPCPDRWWKGNHCCYFSYEEDWNNSLEFCLARDSHLVLITQNQEMS 120  
 61 CGGSKGEMCSQSRCPNLMRNGSHCYFSMEKRDNSSLFCADKGSHLTLFPDNQGVN 120

Db 61 CGGSKGEMCSQSRCPNLMRNGSHCYFSMEKRDNSSLFCADKGSHLTLFPDNQGVN 120

QY 121 LLQVFELSEAFCWIGLRLNNSGWRWEDGSPLNFSRISSNSFYQTQCGAINKNGLQASSCEVPL 180  
 121 LFQEYXGDFTWIGLRDIDGRWEDGPALSLS-ILSNNSVYQKCGTTHRCGLHASSCEVAL 179

QY 121 LLQVFELSEAFCWIGLRLNNSGWRWEDGSPLNFSRISSNSFYQTQCGAINKNGLQASSCEVPL 180  
 121 LFQEYXGDFTWIGLRDIDGRWEDGPALSLS-ILSNNSVYQKCGTTHRCGLHASSCEVAL 179

QY 181 HGVCKKV 187  
 :|||  
 Db 180 QWICKKV 186

|   |                                     |    |                  |
|---|-------------------------------------|----|------------------|
| Db  | 180 QWICKEKV 186                    | Qy | 181 HGVCKKV 187  |
| <b>RESULT 7</b>   |                                     |    |                  |
| ID AAE11761   | AAE11761 standard; protein; 188 AA. | Db | 180 QWICKEKV 186 |
| XX  |                                     |    |                  |
| AC AAE11761;  |                                     |    |                  |
| XX DT 18-DEC-2001 (first entry)   |                                     |    |                  |
| XX DE Rat mast cell function associated antigen (MAFA) protein.   |                                     |    |                  |
| XX XX   |                                     |    |                  |
| XX KW pharmaceutical composition, mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.  |                                     |    |                  |
| XX KW Rattus norvegicus.  |                                     |    |                  |
| XX OS WO200170805-A2.   |                                     |    |                  |
| XX PD 27-SEP-2001.  |                                     |    |                  |
| XX PF 16-MAR-2001; 2001WO-US008596.   |                                     |    |                  |
| XX PR 17-MAR-2000; 2000US-0190716P.   |                                     |    |                  |
| XX PA (GEMI-) GEMINI SCI INC.   |                                     |    |                  |
| XX PI Takahashi N, Mikayama T;  |                                     |    |                  |
| XX DR WPI; 2001-611482/70.  |                                     |    |                  |
| XX DR N-PSDB; AADI8736.   |                                     |    |                  |
| PT Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.  |                                     |    |                  |
| PT PT   |                                     |    |                  |
| PT PT   |                                     |    |                  |
| XX Example 1; Page 19; 49pp; English.   |                                     |    |                  |
| XX The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting on NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAFA protein |                                     |    |                  |
| XX Sequence 188 AA;   |                                     |    |                  |
| Qy 51.4%; Score 525.5; DB 4; Length 188;  |                                     |    |                  |
| Best Local Similarity 53.5%; Pred. No. 1-7e-46;   |                                     |    |                  |
| Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;  |                                     |    |                  |
| Qy 1 MTDSVIYSMLELPTATOQNDYGPQQKSSSKPSCSCLVAITGLLTAVLLVQWIL 60   |                                     |    |                  |
| Db 1 MADNSIVTSMLELPTAALAPRQDDSPWKVAVLHRCVSTLWVAGLTVMLLYQRTL 60  |                                     |    |                  |
| Qy 61 CGGSNYSTOASCPSCPDRMKYGNHCHYF SVEEKDNNSLLECLARDSHLVYTIDNQEMS 120   |                                     |    |                  |
| Db 61 CCGSKGPMCSQSRCRPNLWRIGSHCYFSMERRDWSLKLCAKDSLTLTEPDNQGVN 120   |                                     |    |                  |
| Qy 121 LLQVFLSEAFCWIGLRNNSGWRMEDGSPLNFSSNSFVQPGAIKNKGLOASSCEVPL 180   |                                     |    |                  |
| Qy 121 LFQEYVGDFPYWGLRDIDGWMDGPALSLS-ILSNNSVQXCGTIHRCGLHASSCEVNL 179  |                                     |    |                  |
| Db 121 ISSNSFVOTCGATTGHIQASSCEVPL 64 -----  |                                     |    |                  |
| Qy 181 HGVCKKVRL 189  |                                     |    |                  |
| <b>RESULT 8</b>   |                                     |    |                  |
| ID AAW88267   | AAW88267 standard; protein; 99 AA.  | Db | 180 QWICKEKV 186 |
| XX DT 29-MAR-1999 (first entry)   |                                     |    |                  |
| XX DE Human MAFA splice variant humMAFA (E3/4-).  |                                     |    |                  |
| XX KW Mast cell function-associated antigen; MAFA; humMAFA (E3/4-); splice variant; human; inflammation; asthma; rheumatoid arthritis; tumour; therapy.   |                                     |    |                  |
| XX OS Homo sapiens.   |                                     |    |                  |
| XX PN WO9854209-A2.   |                                     |    |                  |
| XX PD 03-DEC-1998.  |                                     |    |                  |
| XX PF 29-MAY-1998; 98WO-GB001572.   |                                     |    |                  |
| XX PR 31-MAY-1997; 97GB-00011148.   |                                     |    |                  |
| XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.   |                                     |    |                  |
| XX PI Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  |                                     |    |                  |
| XX DR WPI; 1999-059806/05.  |                                     |    |                  |
| XX DR N-PSDB; AAV84200.   |                                     |    |                  |
| PT New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.  |                                     |    |                  |
| PT PT   |                                     |    |                  |
| PT PS Disclosure; Fig 3; 44pp; English.   |                                     |    |                  |
| XX This is the amino acid sequence of human mast cell function-associated antigen (MAFA) splice variant humMAFA (E3/4-), which lacks the C-lectin-like domain of human MAFA (see AAW88265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail.  |                                     |    |                  |
| CC Truncated MAFA polypeptides including humMAFA (E3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88288-72), can be used in compositions for the treatment of CC inflammatory and allergic diseases (e.g. rheumatoid arthritis and CC asthma), or tumour growth   |                                     |    |                  |
| XX Sequence 99 AA;  |                                     |    |                  |
| Qy 42.1%; Score 431; DB 2;  |                                     |    |                  |
| Best Local Similarity 50.3%; Pred. No. 5.4e-3;  |                                     |    |                  |
| Matches 95; Conservative 1; Mismatches 3; Indels 90; Gaps 1;  |                                     |    |                  |
| Qy 1 MTDSVIYSMLELPTATOQNDYGPQQKSSSKPSCSCLVAITGLLTAVLLVQWIL 60   |                                     |    |                  |
| Db 1 MTDSVIYSMLELPTAQNDYGPQQKSSSKPSCSCLVAITGLLTAVLLVQWIL 60   |                                     |    |                  |
| Qy 61 CGGSNYSTOASCPSCPDRMKYGNHCHYF SVEEKDNNSLLECLARDSHLVYTIDNQEMS 120   |                                     |    |                  |
| Db 61 CCGSKGPMCSQSRCRPNLWRIGSHCYFSMERRDWSLKLCAKDSLTLTEPDNQGVN 120   |                                     |    |                  |
| Qy 121 LLQVFLSEAFCWIGLRNNSGWRMEDGSPLNFSSNSFVQPGAIKNKGLOASSCEVPL 180   |                                     |    |                  |
| Qy 121 ISSNSFVOTCGATTGHIQASSCEVPL 64 -----  |                                     |    |                  |
| Qy 181 HGVCKKVRL 189  |                                     |    |                  |

|                              |  |  |
|------------------------------|--|--|
| Db                           | <br>91 HWVCKXVRL 99  | KW<br>KW<br>Homo sapiens.  |
|                              | RESULT 9   | OS   |
|                              | AAR77472   | XX   |
| ID                           | AAR77472 standard; protein; 114 AA.  | NN   |
| XX                           |  | NN   |
| AC                           | AAR77472;  | PN   |
| XX                           |  | W09854209 A2.  |
| DT                           | 01-FBB-1996 (first entry)  | XX   |
| XX                           |  | PD 03-DEC-1998.  |
| DE                           | Partial sequence of mast cell function-associated antigen (MAFA).  | XX   |
| XX                           |  | XX 29-MAY-1998; 98WO-GB001572.   |
| XX                           | Mast cell function-associated antigen; MAFA; soluble; ligand; allergy; allergic; identification; screening; inflammatory; prevention.  | XX 31-MAY-1997; 97GB-00011148.   |
| KW                           | Rattus rattus.   | XX (PEPT-) PEPTIDE THERAPEUTICS LTD.   |
| XX                           |  | PA   |
| OS                           | W09527734-A1.  | XX   |
| XX                           |  | PI   |
| PN                           | YEDA RES & DBV CO LTD.   | XX Hewitt EL, Lamers MBAC, Lamont A, Williams DH;  |
| XX                           | (RYCU/)  | XX DR 1999-059806/05.  |
| PD                           | 19-OCT-1995.   | DR N-PSDB; AAV84199.   |
| XX                           |  | XX   |
| PP                           | 06-APR-1995; 95WO-US004258.  | PT New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.   |
| XX                           |  | PT Disclosure; Fig 2; 4pp; English.  |
| PS                           | 08-APR-1994; 94IL-00109257.  | PT   |
| XX                           |  | CC This is the amino acid sequence of human mast cell function-associated antigen (MAFA) splice variant humMAFA(E3-). humMAFA(E3-) is a major transcript, not found in rat, but highly expressed in human lung and granulocyte-enriched blood cells. The truncated protein includes the intracellular and transmembrane regions of human MAFA (see AAW8264), followed immediately by a polyproline motif (see AAW8264) due to a reading frameshift. This unique motif has been used to design peptides (see AAW8259-64, AAW8268-72) that inhibit human T cell antigen receptor-dependent activation induced by interleukin-2 (IL2) secretion from human Jurkat T cells or IgE dependent degranulation of rat basophil leukaemic cells. Inhibition of IL2 production prevents T cell proliferation and suppresses the immune system. These peptides, truncated MAFA polypeptides including humMAFA(E3-), and polymucleotides encoding them, can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth. |
| DR                           | 1995-366356/47.  | CC   |
| XX                           |  | CC Sequence 70 AA;   |
| DR                           | N-PSDB; AAT0147L.  | CC   |
| XX                           |  | Query Match 30.0%; Score 306.5; DB 2; Length 70;   |
| PT                           | Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.   | Best Local Similarity 82.9%; Pred. No. 3.5e-24;  |
| PT                           |  | Matches 63; Conservative 1; Mismatches 5; Indels 7; Gaps 1;  |
| Pecht I, Guthmann MD, Tal M; |  | Qy 1 MTDSVIYSMELPATAQNDYGPQQKSSSSPKPSCSCLVIAITLGILTAVLLSVLYQWL 60  |
| XX                           |  | Db 1 MTDSVIYSMELPATAQNDYGPQQKSSSSRPSCSCLVIALGILTAVLLSVLYQWL 60   |
| DR                           | WPI; 1995-366356/47.   | Qy 61 CQGSNYSCTASCSCPSCP 76  |
| XX                           |  | Db 61 CQ-----EPAPSPP 69  |
| PS                           | Page 38; 54pp; English.  | RESULT 11  |
| XX                           |  | AAM14192   |
| CC                           | A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions | XX   |
| CC                           | Sequence 114 AA;   | XX   |
| XX                           |  | XX 12-OCT-2001 (first entry)   |
| SQ                           | Query Match 36.2%; Score 370.5; DB 2; Length 114;  | XX   |
|                              | Best Local Similarity 58.4%; Pred. No. 1.4e-30;  | XX   |
|                              | Matches 66; Conservative 18; Mismatches 28; Indels 1; Gaps 1;  | XX   |
| Qy                           | 75 CPDRMKYGNHCYYFVEEKDNWNSLSEFICARDSHSLVLTIDNQEMSLLOVFLSEAFCWIG 134  | DE Peptide #626 encoded by probe for measuring cervical gene expression.   |
| Db                           | 1 CPNLWNRGSHCYYSFMSERDWNSLSEFKADKGSHLTFFDNQVNLFQEYVGDFYWIG 60  | XX Probe; human; microarray; gene expression; cervical epithelial cell;  |
| Qy                           | 135 LRNNNSWRWEWGSPANFSRSNSNFSQTCGAINKNGLQASSCEVPLHGVCKV 187  | XX cervical cancer.  |
| Db                           | 61 LRDIDGRWRWEDGPALSL-TLSNSVYQRCGTIHRCGLASSCEVALQWICBKV 112  | XX Homo sapiens.   |
| RESULT 10                    |  | OS   |
| ID                           | AAW88266 standard; protein; 70 AA.   | AC AAM14192;   |
| XX                           |  | AC   |
| AC                           | AAW88266;  | XX   |
| XX                           | 29-MAR-1999 (first entry)  | DE   |
| DT                           | Human MAFA splice variant humMAFA (E3-).   | XX   |
| XX                           | Mast cell function-associated antigen; MAFA; humMAFA (E3-); splice variant;  | DE   |
| KW                           |  | XX   |

PN WO200157278-A2.  
 XX 09-AUG-2001.  
 XX 30-JAN-2001; 2001WO-US000670.  
 XX PF  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-02363236.  
 XX PR 03-AUG-2000; 2000US-00608408.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-483447/52.  
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX PT gene expression in human foetal liver.  
 XX PS Claim 27; SEQ ID NO 25774; 639pp + Sequence Listing; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human foetal liver. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid probe  
 CC of the invention. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
 XX SQ Sequence 35 AA;  
 Query Match Score 217; DB 4; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-15;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 Qy 64 SNYSTCASCPSCPDRWKYGNHCYYFSVEEKDWN 98  
 Db 1 SNYSTCASCPSCPDRWKYGNHCYYFSVEEKDWN 35  
 XX  
 RESULT 13  
 ID AAM26602 standard; protein; 35 AA.  
 XX  
 AC AAM26602;  
 XX DT 17-OCT-2001 (First entry)  
 DE Peptide #639 encoded by probe for measuring placental gene expression.  
 XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
 XX KW genetic disorder.  
 XX OS Homo sapiens.  
 XX PN WO200157277-A2.  
 XX PD 09-AUG-2001.  
 XX XX 30-JAN-2001; 2001WO-US000663.  
 XX PF  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-488897/53.  
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX PT gene expression in human Placenta.  
 XX PS  
 XX  
 CC Claim 27; SEQ ID NO 26871; 654pp; English.

The present invention relates to single exon nucleic acid probes (SENPs; see AA13135-AA15746). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human Placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

XX Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.1e-15;  
Matches 35; Conservative 0; Mismatches 0;  
DB 64 SNYSTCASCPSCPDRMKYGNHCYTFSEEKDWNS 98  
Qy 1 SNYSTCASCPSCPDRMKYGNHCYTFSEEKDWNS 35  
Db

RESULT 14  
ABB27967 standard; Peptide; 35 AA.  
XX ABB27967;  
XX DT 01-FEB-2002 (first entry)  
XX Human Peptide #618 encoded by breast cell single exon nucleic acid probe.  
XX Human; microarray; single exon probe; gene expression; breast; disease; cancer.  
XX Homo sapiens.  
XX PN WO200157271-A2.  
XX PD 09-AUG-2001.  
XX PP 30-JAN-2001; 2001WO-US000662.  
XX PR 04-FEB-2000; 2000US-01B0312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-0207456P.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0234687P.  
PR 04-OCT-2000; 2000US-0234687P.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA XX DR 2001-496933/54.  
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX PS New spatially-addressable set of single exon nucleic acid probes, useful  
PT for measuring gene expression in sample derived from human breast,  
PT comprises number of single exon nucleic acid probes.

PS Claim 27; SEQ ID NO 10935; 32pp + Sequence Listing; English.  
XX The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human breast and BT 474 cells. The method involves contacting the  
CC probes with a collection of detectably labelled nucleic acids derived  
CC from mRNA of human breast, and then measuring the label bound to each  
CC probe of the microarray. The probes are useful for verifying the  
CC expression of regions of genomic DNA predicted to encode proteins. They  
CC are useful for gene discovery, and for determining predisposition and/or  
CC diagnosing breast disease. Gene expression analysis is useful for  
CC assessing the toxicity of chemical agents on cells. The microarray of  
CC this invention presents a far greater diversity of probes for measuring  
CC gene expression, with far less bias than expressed sequence tag  
CC microarrays. The method is suitable for rapid production of functional  
CC information from genomic sequence. The present sequence is a peptide

CC encoded by a single exon nucleic acid probe of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 35 AA;

Query Match 21.2%; Score 217; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.1e-15;  
Matches 35; Conservative 0; Mismatches 0;  
DB 64 SNYSTCASCPSCPDRMKYGNHCYTFSEEKDWNS 98  
Qy 1 SNYSTCASCPSCPDRMKYGNHCYTFSEEKDWNS 35  
Db

RESULT 15  
ABB18604  
ID ABB18604 standard; protein; 35 AA.  
XX AC ABB18604;  
AC ABB18604;  
XX DT 23-JAN-2002 (first entry)  
XX DE Protein #603 encoded by probe for measuring heart cell gene expression.  
XX KW Human; gene expression; heart; microarray; vascular system;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease.  
XX OS Homo sapiens.  
XX PN WO200157274-A2.  
XX PD 09-AUG-2001.  
XX PP 30-JAN-2001; 2001WO-US000666.  
XX PR 04-FEB-2000; 2000US-01B0312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-0207456P.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0234687P.  
PR 04-OCT-2000; 2000US-0234687P.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA XX DR 2001-488899/53.  
XX PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts.  
XX PS Claim 15; SEQ ID NO 20374; 530pp; English.  
XX DR WPI; 2001-488899/53.

CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart (see  
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
CC probe. The probes may be used for predicting, measuring and displaying  
CC gene expression in samples derived from the human heart via microarrays.  
CC By measuring gene expression, the probes are useful for predicting,  
CC diagnosing, grading, staging, monitoring and prognosis diseases of the  
CC human heart and vascular system e.g. cardiovascular disease,  
CC hypertension, cardiac arrhythmias and congenital heart disease.  
CC Note: The specification data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 35 AA;  
Query Match 21.2%; Score 217; DB 4; Length 35;

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Best Local Similarity 100.0%; Pred. No. 3.1e-15;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 64 SNEYTCASCPSCPSCDRWMKYGNHCCYYFSYERKDWN 98  
Db 1 SNEYTCASCPSCPSCDRWMKYGNHCCYYFSYERKDWN 35

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OM protein - protein search, using sw model

Run on: August 10, 2004, 16:35:05 ; Search time 53 Seconds  
(without alignments)  
1118.605 Million cell updates/sec

Title: US-09-811-367B-1  
Perfect score: 1023  
Sequence: 1 MTDVIYSSMLEPTATQAQN . . . . . GLQASSCEVPLHGVCKKVR1 189

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 727970

Minimum DB seq length: 0  
Maximum DB seq length: 189

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
 1: /cgn2\_6\_ptodata/2/pubpaas/us07\_pubcomb.pep:  
 2: /cgn2\_6\_ptodata/2/pubpaas/us06\_pubcomb.pep:  
 3: /cgn2\_6\_ptodata/2/pubpaas/us06\_new\_pub.pep:  
 4: /cgn2\_6\_ptodata/2/pubpaas/us06\_pubcomb.pep:  
 5: /cgn2\_6\_ptodata/2/pubpaas/us07\_new\_pub.pep:  
 6: /cgn2\_6\_ptodata/2/pubpaas/pctus\_pubcomb.pep:  
 7: /cgn2\_6\_ptodata/2/pubpaas/us08\_new\_pub.pep:  
 8: /cgn2\_6\_ptodata/2/pubpaas/us08\_pubcomb.pep:  
 9: /cgn2\_6\_ptodata/2/pubpaas/us09\_pubcomb.pep:  
 10: /cgn2\_6\_ptodata/2/pubpaas/us09b\_pubcomb.pep:  
 11: /cgn2\_6\_ptodata/2/pubpaas/us09c\_pubcomb.pep:  
 12: /cgn2\_6\_ptodata/2/pubpaas/us09\_new\_pub.pep:  
 13: /cgn2\_6\_ptodata/2/pubbaa/us10a\_pubcomb.pep:  
 14: /cgn2\_6\_ptodata/2/pubbaa/us10b\_pubcomb.pep:  
 15: /cgn2\_6\_ptodata/2/pubbaa/us10c\_pubcomb.pep:  
 16: /cgn2\_6\_ptodata/2/pubbaa/us110\_new\_pub.pep:  
 17: /cgn2\_6\_ptodata/2/pubbaa/us560\_new\_pub.pep:  
 18: /cgn2\_6\_ptodata/2/pubbaa/us660\_pubcomb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT 1  
US-09-811-367B-1  
; Sequence 1, Application US/09811367B  
; Patent No. US09811367B1  
; GENERAL INFORMATION:  
; APPLICANT: GEMINI SCIENCE, INC.  
; ATTORNEY: Takahashi, Nozaki & Associates  
; APPLICANT: Mikayama, Toshihumi  
; TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (M2FA)  
; FILE REFERENCE: 021286/0278719  
; CURRENT APPLICATION NUMBER: US/09/811-367B  
; PRIORITY APPLICATION NUMBER: US/09/811-367B  
; PRIORITY FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO: 1  
; LENGTH: 189  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-811-367B-1

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                  | Description            |
|------------|-------|-------------|--------|------------------------|------------------------|
| 1          | 1023  | 100.0       | 189    | 9 US-09-811-367B-1     | Sequence 1, Appli      |
| 2          | 1007  | 98.4        | 189    | 14 US-10-207-655-196   | Sequence 196, Appli    |
| 3          | 548.5 | 53.6        | 189    | 9 US-09-811-367B-3     | Sequence 3, Appli      |
| 4          | 525.5 | 51.4        | 188    | 9 US-09-811-367B-5     | Sequence 5, Appli      |
| 5          | 217   | 21.2        | 35     | 9 US-09-864-761-33902  | Sequence 33902, Appli  |
| 6          | 216.5 | 21.2        | 182    | 14 US-09-764-870-310   | Sequence 310, Appli    |
| 7          | 216.5 | 21.2        | 182    | 14 US-10-125-540-310   | Sequence 310, Appli    |
| 8          | 196.5 | 19.2        | 179    | 10 US-09-919-039-130   | Sequence 130, Appli    |
| 9          | 196.5 | 19.2        | 179    | 15 US-10-333-009-110   | Sequence 10, Appli     |
| 10         | 175   | 17.1        | 149    | 10 US-09-284-320-11    | Sequence 11, Appli     |
| 11         | 175   | 17.1        | 149    | 13 US-10-114-893-32    | Sequence 32, Appli     |
| 12         | 175   | 17.1        | 149    | 14 US-10-088-859-2     | Sequence 2, Appli      |
| 13         | 175   | 17.1        | 149    | 14 US-10-179-528-1     | Sequence 1, Appli      |
| 14         | 168.5 | 16.5        | 95     | 12 US-10-124-599-22218 | Sequence 222182, Appli |
| 15         | 168   | 16.4        | 149    | 9 US-09-944-807-6      | Sequence 6, Appli      |

RESULT 2  
US-10-207-55-196  
Sequence 196, Application US/10207655  
Publication No. US2003011859A1  
GENERAL INFORMATION:  
APPLICANT: Ledbetter, Jeffrey A.  
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
FILE REFERENCE: 390069\_401C1  
CURRENT APPLICATION NUMBER: US/10/207, 655  
NUMBER OF SEQ ID NOS: 426  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 196  
LENGTH: 189  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-207-55-196

Query Match 98.4%; Score 1007; DB 14; Length 189;  
Best Local Similarity 98.4%; Pred. No. 1 6e-95; 2; Indels 0; Gaps 0;  
Matches 186; Conservative 1; Mismatches 1;

Qy 1 MTDSVIVSMLELPTAQNDYGPQQKSSSKPSCSCLVATIIGLITAVILSVLYQWIL 60  
Db 1 MTDSVIVSMLELPTAQNDYGPQQKSSSRPSCSCLVATIIGLITAVILSVLYQWIL 60

Qy 61 CGGSNYSTCACSPSCPSPDRMKYGNHCVYFSVEEKDWNSSLFCLARSHLLVITDQEMS 120  
Db 61 CGGSNYSTCACSPSCPSPDRMKYGNHCVYFSVEEKDWNSSLFCLARSHLLVITDQEMS 120

Qy 121 LLOVFLSEAFCWIGLRNNSGWRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180  
Db 121 LLOVFLSEAFCWIGLRNNSGWRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180

Qy 181 HGVCCKVRL 189  
Db 181 HWVCKVRL 189

RESULT 3  
US-09-811-367B-3  
Sequence 3, Application US/09811367B  
GENERAL INFORMATION:  
APPLICANT: GEMINI SCIENCE, INC.  
APPLICANT: Takahashi, No. US20020155110A1  
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM  
FILE REFERENCE: 021286/0278719  
CURRENT APPLICATION NUMBER: US/09/811, 367B  
PRIORITY FILING DATE: 2002-03-12  
PRIORITY NUMBER: 60/190, 716  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 188  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-811-367B-5

Query Match 51.4%; Score 525.5; DB 9; Length 188;  
Best Local Similarity 53.5%; Pred. No. 6.7e-46; 5; Indels 1; Gaps 1;  
Matches 100; Conservative 29; Mismatches 57;

Qy 1 MTDSVIVSMLELPTAQNDYGPQQKSSSKPSCSCLVATIIGLITAVILSVLYQWIL 60  
Db 1 MADSIVTSLLEPAAPRYODDSERWKVAVLHRECVSYLVMVALGLITVILMSLLYQWIL 60

Qy 61 CGGSNYSTCACSPSCPSPDRMKYGNHCVYFSVEEKDWNSSLFCLARSHLLVITDQEMS 120  
Db 61 CGCSKGPMQSQCRCPCPNLMWNRNSHCVYFSMEKRDWNSSLKEADKGSHLLTPDNQGVN 120

Qy 121 LLOVFLSEAFCWIGLRNNSGWRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180  
Db 121 LLOVFLSEAFCWIGLRNNSGWRMEDGSPLNFSRISNSFVQTGAINKNGLQASSCEVPL 180

Qy 181 HGVCCKV 187  
Db 180 QWICEKV 186

RESULT 5  
US-09-864-761-33902  
Sequence 3902, Application US/09864761  
Patent No. US2002004763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Shannon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenshang  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1

Query Match 53.6%; Score 548.5; DB 9; Length 188;  
Best Local Similarity 55.6%; Pred. No. 2.9e-48; 26; Mismatches 56; Indels 1; Gaps 1;

CURRENT APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00660  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203  
 PRIOR FILING DATE: 2001-01-29  
 NUMBER OF SEQ ID NOS: 49117  
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 SEQ ID NO 33902  
 LENGTH: 35  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: MAP TO AC0074:6.1  
 OTHER INFORMATION: EXPRESSED IN BT474,  
 OTHER INFORMATION: EXPRESSED IN BRAIN,  
 SIGNAL = 4.7  
 OTHER INFORMATION: EXPRESSED IN HEART,  
 SIGNAL = 8.9  
 OTHER INFORMATION: EXPRESSED IN BONE MARROW,  
 SIGNAL = 6.3  
 OTHER INFORMATION: EXPRESSED IN PLACENTA,  
 SIGNAL = 18  
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER,  
 SIGNAL = 22  
 OTHER INFORMATION: EXPRESSED IN HELA,  
 SIGNAL = 8  
 OTHER INFORMATION: EXPRESSED IN LUNG,  
 SIGNAL = 1.3  
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER,  
 SIGNAL = 30  
 OTHER INFORMATION: EXPRESSED IN HBL100,  
 SIGNAL = 6.1  
 OTHER INFORMATION: EST HUMAN HIT: BF241894:1,  
 EVALUATE 4.00e-15  
 OTHER INFORMATION: EST HUMAN HIT: AA188327:1,  
 EVALUATE 1.00e-14  
 US-09-864-761-33902

Query Match 64 SNYSTCACSPSCDPDRMKGNHCCYFSYEKWDNS 98  
 Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 SNYSTCACSPSCDPDRMKGNHCCYFSYEKWDNS 35

Patent No. US20020042386A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PTZL4  
 CURRENT APPLICATION NUMBER: US/09/764,870  
 CURRENT FILING DATE: 2001-01-17  
 Prior application data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 646  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 310  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-764-870-310

Query Match 64 SNYSTCACSPS----CPDRMMKGNHCCYFSYEKWDNS 21.2%; Score 216.5; DB 9; Length 182;  
 Best Local Similarity 35.0%; Pred. No. 4.6e-14;  
 Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

Qy 64 SNYSTCACSPS----CPDRMMKGNHCCYFSYEKWDNS 21.2%; Score 216.5; DB 9; Length 182;  
 Db 49 SNKDLCAERSADQTVLQSEWLYQGKCYWFNSNEKMSDSYVCLERKSHLILHDQE 11.6  
 Qy 119 MSLLQVLFSEA-FCWIGLRNNS --GWRWEDGSPLNFRISSNSFVQ----TCGAIK 168  
 Db 109 MAFIQNURQLNVIWIGNFTSLKMTWVWDGSPID---SKIFFRGPRAKENSRAIKE 164  
 Qy 169 NGLOASSCEVPLHGVCK 185  
 Db 165 SKIFSETCSSVFKWICQ 181

RESULT 7  
 US-10-125-540-310  
 Sequence 310, Application US/10125540  
 Publication No. US20030059875A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PTZL4C1  
 CURRENT APPLICATION NUMBER: US/10/125,540  
 CURRENT FILING DATE: 2002-04-19  
 Prior application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 646  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 310  
 LENGTH: 182  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-125-540-310

Query Match 64 SNYSTCACSPS----CPDRMMKGNHCCYFSYEKWDNS 21.2%; Score 216.5; DB 14; Length 182;  
 Best Local Similarity 35.0%; Pred. No. 4.6e-14;  
 Matches 48; Conservative 22; Mismatches 48; Indels 19; Gaps 5;

Qy 64 SNYSTCACSPS----CPDRMMKGNHCCYFSYEKWDNS 21.2%; Score 216.5; DB 14; Length 182;  
 Db 49 SNKDLCAERSADQTVLQSEWLYQGKCYWFNSNEKMSDSYVCLERKSHLILHDQE 11.6  
 Qy 119 MSLLQVLFSEA-FCWIGLRNNS --GWRWEDGSPLNFRISSNSFVQ----TCGAIK 168  
 Db 109 MAFIQNURQLNVIWIGNFTSLKMTWVWDGSPID---SKIFFRGPRAKENSRAIKE 164  
 Qy 169 NGLOASSCEVPLHGVCK 185  
 Db 165 SKIFSETCSSVFKWICQ 181

RESULT 8  
 US-09-919-039-130  
 Sequence 310, Application US/09919039  
 Publication No. US20030108871A1

RESULT 6  
 US-09-764-870-310  
 Sequence 310, Application US/09764870

GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R. EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; TITLE OF INVENTION: PA-0335 US  
; FILE REFERENCE: CURRENT PELLITION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program.  
; SEQ ID NO: 130  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1  
; US-09-919-039-130

Query Match 35 CSCLVAVITGLLAVLSSLYQWLQGSN--YSTCASCPCSPCDRWMKYGHNHCYXFYSVE 92  
Best Local Similarity 32.7%; Score 196.5; DB 10; Length 179;  
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

US-10-335-009-10

Query Match 35 CSCLVAVITGLLAVLSSLYQWLQGSN--YSTCASCPCSPCDRWMKYGHNHCYXFYSVE 92  
Best Local Similarity 32.7%; Score 196.5; DB 15; Length 179;  
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

RESULT 9  
US-10-335-009-10  
; Sequence 10, Application US/10335009  
; Publication No. US2004000180A1  
; GENERAL INFORMATION:  
; APPLICANT: Porunelloor , Mathew A.  
; INVENTION: Boles, Kent S.  
; TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION  
; FILE REFERENCE: 11707.02/46687-7  
; CURRENT APPLICATION NUMBER: US/10/335.009  
; CURRENT FILING DATE: 2002-12-31  
; PRIOR APPLICATION NUMBER: US 09/475,365  
; PRIOR FILING DATE: 1999-12-30  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 10  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-335-009-10

Query Match 93 EKDWNSSLEFLCLARDSHLLVITDNQEMSLLQVFLSEAFWIGL--RNNSGMRWEQDGSPL 149  
Best Local Similarity 32.2%; Score 196.5; DB 15; Length 179;  
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

RESULT 10  
US-09-284-320-11  
; Sequence 11, Application US/09284320  
; Publication No. US20030092175A1  
; GENERAL INFORMATION:  
; APPLICANT: Kato, Seishi et al.  
; INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs  
; TITLE OF INVENTION: ENCODING THESE PROTEINS  
; FILE REFERENCE: GIN-6705CPUS  
; CURRENT APPLICATION NUMBER: US/09/284,320  
; CURRENT FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: JP 8-301429  
; PRIOR FILING DATE: 1996-11-13  
; PRIOR APPLICATION NUMBER: PCT/JP97/04056  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 11  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-284-320-11

Query Match 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Db 35 CPYDWIGFQNHCYXFKEEGIWNNSKYNCSQTHADLTIDNIEMNFLRXTKCSSDHWIG 94

Query Match 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Db 95 LKMAKRNRTG-QWVDGA-TFPXSGMRGSEGCAVLSDDGATARTCYTERKWKIRK 146

RESULT 11  
US-10-114-893-32  
; Sequence 32, Application US/10114893  
; Publication No. US2002193567A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; INVENTION: McCoy, John M.  
; TITLE OF INVENTION: McCoy, John M.  
; FILE REFERENCE: CLARSHLLVITDNQEMSLLQVFLSEAFWIGL--RNNSGMRWEQDGSPL 149  
; CURRENT APPLICATION NUMBER: US/09/284,320  
; CURRENT FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: JP 8-301429  
; PRIOR FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 11  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-114-893-32

Query Match 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Db 35 CPYDWIGFQNHCYXFKEEGIWNNSKYNCSQTHADLTIDNIEMNFLRXTKCSSDHWIG 94

Query Match 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Db 95 LKMAKRNRTG-QWVDGA-TFPXSGMRGSEGCAVLSDDGATARTCYTERKWKIRK 146

RESULT 12  
US-10-114-893-32  
; Sequence 32, Application US/10114893  
; Publication No. US2002193567A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; INVENTION: McCoy, John M.  
; TITLE OF INVENTION: McCoy, John M.  
; FILE REFERENCE: CLARSHLLVITDNQEMSLLQVFLSEAFWIGL--RNNSGMRWEQDGSPL 149  
; CURRENT APPLICATION NUMBER: US/09/284,320  
; CURRENT FILING DATE: 1999-06-21  
; PRIOR APPLICATION NUMBER: JP 8-301429  
; PRIOR FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 12  
; LENGTH: 149  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-114-893-32

Query Match 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 75 CPDRWMKYGHNHCYXFYSVEEKDNQEMSLLQVFLSEAFWIG 134  
Db 35 CPYDWIGFQNHCYXFKEEGIWNNSKYNCSQTHADLTIDNIEMNFLRXTKCSSDHWIG 94

Query Match 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Best Local Similarity 32.2%; Score 175; DB 10; Length 149;  
Matches 37; Conservative 24; Mismatches 48; Indels 6; Gaps 3;

Qy 135 D--RNNSGMRWEQDGSPLNSRISSSNSFVQPTGAINRNGLASSCEVPLHGVCKK 186  
Db 95 LKMAKRNRTG-QWVDGA-TFPXSGMRGSEGCAVLSDDGATARTCYTERKWKIRK 146

Db 35 CPYDWIGFQNCKCYYSKEGDNSSKYNSTQHADLTIONEENFLRKYKCSSDHWIG 94  
 Qy 135 L--RNNSGWRWEDGSPLNSRISNSFVQTGAINKNGIQAASSCEVPLHGVCK 186  
 Db 95 LKMAKNRTG-QWVDGA--TFTKSGMRSSECAVLSDDDGAATRCYTERKWCRK 146

RESULT 12

US-10-088-859-2

Sequence 2, Application US/10088859

Publication No. US20030148468A1

GENERAL INFORMATION:

APPLICANT: KATO, Seishi

APPLICANT: NAGATA, Naoki

APPLICANT: FUJIMURA, Naoko

APPLICANT: KOBAYASHI, Midori

APPLICANT: ITO, Kochi

APPLICANT: ISHIZUKA, Yoshiko

TITLE OF INVENTION: A Method For Producing an Antibody by Gene Immunization

FILE REFERENCE: 2002-0400A/LC/00653

CURRENT APPLICATION NUMBER: US10/088,859

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: PCT/JP01/06377-

PRIOR FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: JP2000-222743

PRIOR FILING DATE: 2000-07-24

PRIOR APPLICATION NUMBER: JP2000-254407

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 149

TYPE: PRY

ORGANISM: Homo sapiens

US 10-088-859-2

Query Match

Best Local Similarity 32.2%;

Score 175; DB 14;

Length 149;

Pred. No. 6.be-10;

Indels 6;

Gaps 3;

RESULT 14

US-10-124-599-222182

Sequence 222182, Application US/10424599

Publication No. US2004031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalec, David K

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 222182

LENGTH: 95

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1).195)

OTHER INFORMATION: unsure at all xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_4265C.1.pep

US-10-424-599-222182

Query Match

Best Local Similarity 39.4%;

Score 168.5; DB 12;

Length 95;

Matches 33; Conservative 16; Mismatches 26; Indels 9; Gaps 3;

Qy 67 STCASSCPSCPDWPKGNHCVYFSVEKDWNSSLEFCCLARDSHLIVITDQNQEMSLLQVFL 126

Db 10 SSCA---CLEWKIRHQCSXCFISKEKSMGSREFACSONSSQLQTRNELSFMS--S 63

FILING DATE: 24-Jun-2002

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/846,523

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE DOCKET NUMBER: PF-0281-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEX: 415-845-4166

&gt;&lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 149 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PITUNOT03

CLONE: 1756224

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-179-528-1

Query Match

Best Local Similarity 32.2%;

Score 175; DB 14;

Length 149;

Pred. No. 6.e-10;

Indels 6;

Gaps 3;

RESULT 14

US-10-124-599-222182

Sequence 222182, Application US/10424599

Publication No. US2004031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J

APPLICANT: Kovalec, David K

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 222182

LENGTH: 95

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1).195)

OTHER INFORMATION: unsure at all xaa locations

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_4265C.1.pep

US-10-424-599-222182

Query Match

Best Local Similarity 39.4%;

Score 168.5; DB 12;

Length 95;

Matches 33; Conservative 16; Mismatches 26; Indels 9; Gaps 3;

Qy 67 STCASSCPSCPDWPKGNHCVYFSVEKDWNSSLEFCCLARDSHLIVITDQNQEMSLLQVFL 126

Db 10 SSCA---CLEWKIRHQCSXCFISKEKSMGSREFACSONSSQLQTRNELSFMS--S 63

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RESULT 15
US-09-944-807-6
; Sequence 6, Application US/09944807
; Patent No. US2002011949A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma I
; TITLE OF INVENTION: Method for identifying
; TITLE OF INVENTION: influence inflammatory
; TITLE OF INVENTION: inflammatory airway
; FILE REFERENCE: 082_00n
; CURRENT APPLICATION NUMBER: US/09/944,81
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK/0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
; US/09-944-807-6

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|                       |       |                  |                |
|-----------------------|-------|------------------|----------------|
| Query Match           | 16.4% | Score 168, DB 9; | Length 149     |
| Best Local Similarity | 31.3% | Pred. NO. 3      | 6-e-0;         |
| Matches               | 36:   | Conservative     | Mismatches 24; |
|                       |       |                  | Indels 4.9;    |

Search completed: August 10, 2004, 16:40:34  
Total time : 55 secs

| Result No. | Score | Query Match | Length | DB ID | Description                         | SUMMARIES          |   |
|------------|-------|-------------|--------|-------|-------------------------------------|--------------------|---|
| 1          | 525.5 | 51.4        | 188    | 3     | US-08-722-126A-5                    | Sequence 5, Appli  | Copyright (c) 1993 - 2004 Compugen Ltd.                       |
| 2          | 525.5 | 51.4        | 188    | 5     | PCT-US95-04258-5                    | Sequence 5, Appli  | GenCore version 5.1.6   |
| 3          | 430.0 | 42.0        | 76     | 4     | US-09-531-056A-23                   | Sequence 23, Appli | OM protein - protein search, using sw model                   |
| 4          | 370.5 | 36.2        | 114    | 3     | US-08-722-126A-6                    | Sequence 6, Appli  | Run on: August 10, 2004, 16:32:44 ; Search time 18 Seconds    |
| 5          | 370.5 | 36.2        | 114    | 5     | PCT-US95-04258-6                    | Sequence 6, Appli  | (without alignments)  |
| 6          | 370.5 | 36.2        | 114    | 6     | /cgn2_6/ptodata/2/iaa/6A/COMB.pep:* | Sequence 6, Appli  | 542.073 Million cell updates/sec                              |
| 7          | 196.5 | 19.2        | 179    | 1     | US-08-690-095-9                     | Sequence 9, Appli  | Title: US-09-811-367B-1                                       |
| 8          | 196.5 | 19.2        | 179    | 2     | US-08-688-342-3                     | Sequence 2, Appli  | Perfect score: 1023   |
| 9          | 196.5 | 19.2        | 179    | 2     | US-09-113-788-3                     | Sequence 3, Appli  | Sequence: 1 MDSTVIYSMLEPTATQAQN.....GLQASSCEVPLHGVCCKVKRL 189 |
| 10         | 196.5 | 19.2        | 179    | 3     | US-09-113-789-9                     | Sequence 9, Appli  | Scoring table: BIOSUM62                                       |
| 11         | 175.5 | 17.2        | 168    | 3     | US-08-772-440-17                    | Sequence 17, Appli | Gapop 10.0 , Gapext 0.5                                       |
| 12         | 173   | 16.9        | 175    | 3     | US-08-772-440-15                    | Sequence 15, Appli | Searched: 389414 seqs, 51625971 residues                      |
| 13         | 172   | 16.8        | 134    | 3     | US-08-772-440-16                    | Sequence 16, Appli | Total number of hits satisfying chosen parameters: 303294     |
| 14         | 169.5 | 16.6        | 120    | 3     | US-08-543-246B-18                   | Sequence 18, Appli | Minimum DB seq length: 0                                      |
| 15         | 169.5 | 16.6        | 135    | 3     | US-08-543-246B-17                   | Sequence 17, Appli | Maximum DB seq length: 189                                    |
| 16         | 166   | 16.2        | 134    | 3     | US-08-543-246B-20                   | Sequence 20, Appli | Post-processing: Minimum Match 0%                             |
| 17         | 164.5 | 16.1        | 135    | 3     | US-08-543-246B-19                   | Sequence 19, Appli | Listing First 45 summaries                                    |
| 18         | 162   | 15.8        | 129    | 3     | US-08-722-126A-10                   | Sequence 10, Appli | Issued Patents AA: *  |
| 19         | 162   | 15.8        | 129    | 5     | PCT-US95-04258-10                   | Sequence 10, Appli | 1: /cgn2_6/ptodata/2/iaa/5A/COMB.pep:*                        |
| 20         | 161.5 | 15.8        | 173    | 4     | US-09-531-056A-14                   | Sequence 4, Appli  | 2: /cgn2_6/ptodata/2/iaa/5B/COMB.pep:*                        |
| 21         | 158.5 | 15.5        | 79     | 4     | US-09-531-056A-16                   | Sequence 19, Appli | 3: /cgn2_6/ptodata/2/iaa/6A/COMB.pep:*                        |
| 22         | 158   | 15.4        | 176    | 3     | US-08-772-440-8                     | Sequence 8, Appli  | 4: /cgn2_6/ptodata/2/iaa/6B/COMB.pep:*                        |
| 23         | 158   | 15.4        | 180    | 3     | US-08-772-440-31                    | Sequence 31, Appli | 5: /cgn2_6/ptodata/2/iaa/6C/COMB.pep:*                        |
| 24         | 156.5 | 15.3        | 77     | 4     | US-09-531-056A-22                   | Sequence 22, Appli | 6: /cgn2_6/ptodata/2/iaa/backfiles/1.pep:*                    |
| 25         | 155.5 | 15.2        | 122    | 3     | PCT-US95-04258-9                    | Sequence 9, Appli  | Total number of hits satisfying chosen parameters: 303294     |
| 26         | 155.5 | 15.2        | 122    | 5     | US-08-722-126A-9                    | Sequence 9, Appli  | Post-processing: Maximum Match 100%                           |
| 27         | 155.5 | 15.2        | 187    | 4     | US-09-127-946-12                    | Sequence 12, Appli | Listing First 45 summaries                                    |

## ALIGNMENTS

RESULT 1  
US-08-722-126A-5  
; Sequence 5, Application US/08722126A  
; Patent No. 6034227  
; GENERAL INFORMATION:  
; APPLICANT: PECHT, Israel  
; APPLICANT: GUTHMANN, Marcelo D.  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,126A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109257  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: PECHT=IA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3526  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 188 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; Query Match Score 525.5; DB 3;  
; Best Local Similarity Pred. No. 1.1e-48;  
; US-08-722-126A-5 Length 188;

Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1; Qy 1 MTDSVITYSMELPLTQAQNDYGPQQKSSSSKPKSCSCLVAITGLLTAVLLVLYQWIL 60 Db 1 MADNSIYSTLELPAAPRVQDDSRMKVKAVLHRPCVSYLVVALGTLTILMSLLYQRTL 60 Qy 61 CGGSNYSCTCASCPSCPDRMKXGNHXYCFSYKEWDNNSLLEFLCLARDSHLLVITDQEMS 120 Db 61 CGGSKGFMCQSQRCPNWLWNRGSHYFSMEKRDNNSSLKFCDKGSHLLTPEPNQGYN 120 Qy 121 LLQVELSEAFCWIGLNNSGRWEDGSPLNFSRRISSNSFVOTCGAINKNGLOASSCEVPL 180 Db 121 LFQEYQGDFWYGLRDIDGWRWEDGPAALS-ILNSNVQKCGTHRGHASSCEVAL 179 Qy 181 HGVCCKV 187 Db 180 QWICCKV 186

RESULT 3  
US-09-531-056A-23  
; Sequence 23, Application US/09531056A  
; Patent No. 6455683  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS

Qy 181 HGVCCKV 187  
Db 180 QWICCKV 186

RESULT 2  
PCT-US95-04258-5  
; Sequence 5, Application PC/TUS9504258  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 109257  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25, 618  
; REFERENCE/DOCKET NUMBER: PECHT=1 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3328  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 188 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-04258-5

Query Match 51.4%; Score 525.5; DB 5; Length 188;  
Best Local Similarity 53.5%; Pred. No. 1.1e-48;  
Matches 100; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 1 MTDSVITYSMELPLTQAQNDYGPQQKSSSSKPKSCSCLVAITGLLTAVLLVLYQWIL 60 Db 1 MADNSIYSTLELPAAPRVQDDSRMKVKAVLHRPCVSYLVVALGTLTILMSLLYQRTL 60

Qy 61 CGGSNYSCTCASCPSCPDRMKXGNHXYCFSYKEWDNNSLLEFLCLARDSHLLVITDQEMS 120 Db 61 CGGSKGFMCQSQRCPNWLWNRGSHYFSMEKRDNNSSLKFCDKGSHLLTPEPNQGYN 120

Qy 61 CGGSKGFMCQSQRCPNWLWNRGSHYFSMEKRDNNSSLKFCDKGSHLLTPEPNQGYN 120  
Db 61 CGGSKGFMCQSQRCPNWLWNRGSHYFSMEKRDNNSSLKFCDKGSHLLTPEPNQGYN 120

RESULT 4  
US-08-722-126A-6  
; Sequence 6, Application US/08722126A  
; Patent No. 604227  
; GENERAL INFORMATION:  
; APPLICANT: PECHT, Israel  
; NAME: GUTEMANN, Marcelo D.  
; REFERENCE/DOCKET NUMBER: TAL, Michael  
; TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL  
; TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08722126A  
; FILING DATE: 08-OCT-1996  
; CLASSIFICATION: 536  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04258  
; FILING DATE: 06-APR-1995  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: IL 109257

FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25, 618  
REFERENCE/DOCKET NUMBER: PECHT=1A  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
SEQUENCE FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-722-126A-6

Query Match 36.2%; Score 370.5; DB 5; Length 114;  
Best Local Similarity 58.4%; Pred. No. 2.6e-32;  
Matches 66; Conservative 10; Mismatches 28; Indels 1; Gaps 1;

Qy 75 CPDRWYKGNHCCYFFSVEEKDNNSLLECLARDSHLLVITDNOEMSLQVELSEAFCKV 134  
Db 1 CPNLWNRGSHCCYFFMERDKDNSSRKFADKGSHLLTPDNQGVNLQEVGEDPYWIG 60

Qy 135 LRNNSGMRWEDGSPLNSRISNSFVOTCAINKNG-LQASSCEVPHGVCKV 187  
Db 61 LRIDGMRWEDGPALSLS-TILSNVVOKCGTHRCGLHASSCEVALQWICERKV 112

RESULT 6  
US-08-690-095-9  
Sequence 9, Application US/08690095  
Patient No. 5792648  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Au Young, Janice  
APPLICANT: Goji, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ZIP: 94304  
COUNTRY: U.S.

COMPUTER READABLE FORM:  
MEDIUM TYPE: Disquette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,095  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0110 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1098617  
US-08-690-095-9

Query Match 19.2%; Score 196.5; DB 1; Length 179;  
Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVATLGLLTAVLISVLVQWILCQGSN-YSTCASCSPCDWMMKYGHNHCYFSVE 92  
Db 20 CUSLMA-TLGILLKNSTTKLSTEAPTPGPNTIELQDSDCSQCERWGYRCNCYTSSE 78

Qy 93 EXDNNSLLECLARDSHLLVITDNOEMSLQVELSEAFCKV 149  
Db 79 QKTWNESRHLCAQSQKSLLQLQNTDELFMS-SSOOFWIGLSYSEBETHAWLWNGSAL 136

Qy 150 NFRSRISSNSF---VQTGAINKG-LQASSCEVPHGVCKK 186  
Db 137 -SQYLFPSPFETFTNTKCIATNPNGNALDESCDKNRYICKQ 176

RESULT 7  
US-08-650-578-2  
Sequence 2, Application US/08650578  
Patent No. 58112B4

GENERAL INFORMATION:

APPLICANT: Chang, Chiwen  
APPLICANT: Aramburu Beltran, Jose  
APPLICANT: Lopez-Bonet, Migne J.  
APPLICANT: Phillips Jr., Joseph H.  
APPLICANT: Lanier, Lewis L.

TITLE OF INVENTION: Purified Mammalian NK Antigens and Related Reagents

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.125

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/650,578  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,339  
FILING DATE: 29-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0391  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: protein

US-08-650-578-2

Query Match Score 196.5; DB 2; Length 179;  
Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
Matches 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAITLGLLTAVLLSVLYQWLQGSSN- YSTCACSPSCPDRWMKYGNHCYFSYE 92  
Db 20 CLSINA-TLGILKNSFTKLISIEPAFTPGNTIELQKDSDCCSQQFLQNTDELMIS--SSQQFYTWIGLSYSEHTAWLWNGSAL 136

QY 93 EKDWNSSLECLARDSHLLVITDNGQEMSLLQVFSEAFWIGL--RNNSGWRMEDGSPL 149  
Db 79 QKTWNESRHICASQKSSLQQLQNTDELMIS--SSQQFYTWIGLSYSEHTAWLWNGSAL 136

QY 150 NFSRISNSF---VQTGGAINKNG-LQASSCEVPLHGVCKK 186  
Db 137 -SQYLFPSPSETNTYKNCIAYNPNGNALDESCDKNYICKQ 176

RESULT 8  
US-08-688-342-3  
Sequence 3, Application US/08688342  
Patent No. 5871964

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Goli, Surya K.

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ZIP: 94304

COMPUTER READABLE FORM:

APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ZIP: 94304

COMPUTER READABLE FORM:

COMPUTER: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/688, 342  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-555-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1098616  
US-08-688-342-3

Query Match Score 196.5; DB 2; Length 179;  
Best Local Similarity 32.7%; Pred. No. 2.4e-13;  
Matches 25; Mismatches 69; Indels 15; Gaps 7;

QY 35 CSCLVAITLGLLTAVLLSVLYQWLQGSSN- YSTCACSPSCPDRWMKYGNHCYFSYE 92  
Db 20 CLSINA-TLGILKNSFTKLISIEPAFTPGNTIELQKDSDCCSQQFLQNTDELMIS--SSQQFYTWIGLSYSEHTAWLWNGSAL 136

QY 93 EKDWNSSLECLARDSHLLVITDNGQEMSLLQVFSEAFWIGL--RNNSGWRMEDGSPL 149  
Db 79 QKTWNESRHICASQKSSLQQLQNTDELMIS--SSQQFYTWIGLSYSEHTAWLWNGSAL 136

QY 150 NFSRISNSF---VQTGGAINKNG-LQASSCEVPLHGVCKK 186  
Db 137 -SQYLFPSPSETNTYKNCIAYNPNGNALDESCDKNYICKQ 176

RESULT 9  
US-09-113-788-3  
Sequence 3, Application US/09113788  
Patent No. 596904

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Goli, Surya K.

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,788  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/688,342  
 FILING DATE:  
 ATTORNEY /AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0110 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEX/FAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617  
 US-09-113-788-9

SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617

Query Match 19.2%; Score 196.5; DB 2; Length 179;  
 Best Local Similarity 32.7%; Prod. No. 2.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVATLGLTAVLLSILQCGSN - YSTCASCPSCPDRMKYGNHCYFESV 92  
 Db 20 CLSLMA-TIGLILKNSFLKLSIPEAFTPGPNBLQKSDCCSQCERWVGRNCYFSS 78

Qy 93 EKDWNSSLEFLCLARDSHLVLITDNOEMSLLQVPLSEAFCWIGL -- RNNSGWRWEDGSPL 149  
 Db 79 QKTWNESHLCAQSQSSLQLONTDELFMS - SSQQYIWHGYSSEHTAWLWENGSAL 136

Qy 35 CSCLVATLGLTAVLLSILQCGSN - YSTCASCPSCPDRMKYGNHCYFESV 92  
 Db 20 CLSLMA-TIGLILKNSFLKLSIPEAFTPGPNBLQKSDCCSQCERWVGRNCYFSS 78

Qy 93 EKDWNSSLEFLCLARDSHLVLITDNOEMSLLQVPLSEAFCWIGL -- RNNSGWRWEDGSPL 149  
 Db 79 QKTWNESHLCAQSQSSLQLONTDELFMS - SSQQYIWHGYSSEHTAWLWENGSAL 136

Qy 150 NFSRISNSP --- VQTGAINKNG-LQASSCEVPLHGVCK 186  
 Db 137 --SQYLFFSFETENTNCTAYNPNGLADESCDKRYICKQ 176

RESULT 11  
 US-09-772-440-17  
 Sequence 17, Application US/08772440  
 Patent No. 6046158

GENERAL INFORMATION:  
 APPLICANT: Ariizumi, Kiyoshi  
 ADDRESS: Takashima, Akira  
 TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE LECTINS, DECTIN-1 AND DECTIN-2, COMPOSITIONS AND USES  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 STREET: P. O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/772,440  
 FILING DATE: CONCURRENTLY HEREWITH  
 CLASSIFICATION: 435

GENERAL INFORMATION:  
 PATENT NO. 6034219  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Goli, Surya K.  
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,789  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/690,095

SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617

Query Match 19.2%; Score 196.5; DB 3; Length 179;  
 Best Local Similarity 32.7%; Prod. No. 2.4e-13;  
 Matches 53; Conservative 25; Mismatches 69; Indels 15; Gaps 7;

Qy 35 CSCLVATLGLTAVLLSILQCGSN - YSTCASCPSCPDRMKYGNHCYFESV 92  
 Db 20 CLSLMA-TIGLILKNSFLKLSIPEAFTPGPNBLQKSDCCSQCERWVGRNCYFSS 78

Qy 93 EKDWNSSLEFLCLARDSHLVLITDNOEMSLLQVPLSEAFCWIGL -- RNNSGWRWEDGSPL 149  
 Db 79 QKTWNESHLCAQSQSSLQLONTDELFMS - SSQQYIWHGYSSEHTAWLWENGSAL 136

Qy 35 CSCLVATLGLTAVLLSILQCGSN - YSTCASCPSCPDRMKYGNHCYFESV 92  
 Db 20 CLSLMA-TIGLILKNSFLKLSIPEAFTPGPNBLQKSDCCSQCERWVGRNCYFSS 78

Qy 93 EKDWNSSLEFLCLARDSHLVLITDNOEMSLLQVPLSEAFCWIGL -- RNNSGWRWEDGSPL 149  
 Db 79 QKTWNESHLCAQSQSSLQLONTDELFMS - SSQQYIWHGYSSEHTAWLWENGSAL 136

Qy 150 NFSRISNSP --- VQTGAINKNG-LQASSCEVPLHGVCK 186  
 Db 137 --SQYLFFSFETENTNCTAYNPNGLADESCDKRYICKQ 176

RESULT 10  
 US-09-113-789-9  
 Sequence 9, Application US/09113789  
 GENERAL INFORMATION:  
 PATENT NO. 6034219  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Goli, Surya K.  
 TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 STREET: Incyte Pharmaceuticals, Inc.  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/113,789  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/690,095

SEQUENCE CHARACTERISTICS:  
 LENGTH: 179 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 1098617

LENGTH: 168 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: linear  
 TOPOLOGY: linear

US-08-772-440-17

Query Match Score 175.5; DB 3; Length 168;  
 Best Local Similarity 28.4%; Pred. No. 4e-11;  
 Matches 42; Conservative 28; Mismatches 51; Indels 27; Gaps 4;

Qy 25 QOKSSSSKPSCSCLVAITGLGLTAVILS-----VILYQWILCQS-----NYSTCA 70  
 Db 3 QEROSQKGKVCLWLWSAAVISMLLJSTCFIASCVVTTYQFIMDQSSRRLYELHTYHSSL 62

Qy 71 SCPS-----CPDRNWKYGNHCYYSVEEKDNNSLEFCLARDSHLLVITDNE 118  
 Db 63 TCFSEGTMVSEKMWGCCPNHWKSFSSCYLISTKENFWSTSEQNCVQMGAHLLVVTEAE 122

Qy 119 MSLLOQVFLSEAFCW-IGLRNNSGMRVED 145  
 Db 123 QNFITQNLNESSYFLQNSPKWGD 150

RESULT 12  
 US-08-772-440-15  
 i Sequence 15, Application US/08772440  
 i Patent No. 6046158

GENERAL INFORMATION:  
 i APPLICANT: Arizumi, Kiyoshi  
 i APPLICANT: Takashima, Akira  
 i TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
 i TITLE OF INVENTION: LECTINS, DECINT-1 AND DECINT-2; COMPOSITIONS AND USES  
 i TITLE OF INVENTION: THEREOF  
 i NUMBER OF SEQUENCES: 42  
 i CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: Arnold, White & Durkee  
 i STREET: P.O. Box 4433  
 i CITY: Houston  
 i STATE: Texas  
 i ZIP: 77210

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/772,440  
 i FILING DATE: CONCURRENTLY HEREWITH  
 i CLASSIFICATION: 435  
 i ATTORNEY/AGENT INFORMATION:  
 i NAME: Parker, David L.  
 i REGISTRATION NUMBER: 32,165  
 i TELEPHONE: 512/418-3000  
 i TELEFAX: 512/474-7577  
 i CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/772,440  
 i FILING DATE: CONCURRENTLY HEREWITH  
 i CLASSIFICATION: 435  
 i ATTORNEY/AGENT INFORMATION:  
 i NAME: Parker, David L.  
 i REGISTRATION NUMBER: 32,165  
 i REFERENCE/DOCKET NUMBER: UTXD:493  
 i TELECOMMUNICATION INFORMATION:  
 i TELEPHONE: 512/474-7577  
 i TELEFAX: 512/474-7500  
 i INFORMATION FOR SEQ ID NO: 15:  
 i SEQUENCE CHARACTERISTICS:  
 i LENGTH: 175 amino acids  
 i TYPE: amino acid  
 i STRANDEDNESS:  
 i TOPOLOGY: linear

US-08-772-440-15

Query Match Score 173; DB 3; Length 175;  
 Best Local Similarity 27.7%; Pred. No. 7.e-11;  
 Matches 52; Conservative 34; Mismatches 64; Indels 38; Gaps 9;

Qy 25 QOKSSSSKPSCSCLVAITGLGLTAVILS-----VILCQSNSYTC--ASPS----CPD 77  
 Db 3 QEROSQKGKVCLWLWSAAVISML-----LSTCFIASCVKNGCCPN 47

RESULT 14

Qy 78 RWKXGNHCYYSVEEKDNNSLEFCLARDSHLLVITDNEQEMSLQVFLSEAFCW-IGL- 135  
 Db 48 HWKSFSSCYLISTKENFWSTSEQNCVQMGAHLLVVTEAEQNFTQQLINESYFLGLS 107

Qy 136 --RNNSGMRWEDGSPLN----FSRISSSNFSVQTCGAI----NKNGLQASSCEVPLHGV 183  
 Db 108 DPQNGKQWQMDTDPFSQNVRFWHPHEPNLPEERCVSIVTWNPSKWGNNDVCDSKHNSI 167

Qy 184 C-KKVRL 189  
 Db 168 CEMKKTYL 175

RESULT 13  
 US-08-772-440-16  
 i Sequence 16, Application US/08772440  
 i Patent No. 6046158

GENERAL INFORMATION:  
 i APPLICANT: Arizumi, Kiyoshi  
 i APPLICANT: Takashima, Akira  
 i TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
 i TITLE OF INVENTION: LECTINS, DECINT-1 AND DECINT-2; COMPOSITIONS AND USES  
 i NUMBER OF SEQUENCES: 42  
 i CORRESPONDENCE ADDRESS:  
 i ADDRESSEE: Arnold, White & Durkee  
 i STREET: P.O. Box 4433  
 i CITY: Houston  
 i STATE: Texas  
 i ZIP: 77210

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 i APPLICATION NUMBER: US/08/772,440  
 i FILING DATE: CONCURRENTLY HEREWITH  
 i CLASSIFICATION: 435  
 i ATTORNEY/AGENT INFORMATION:  
 i NAME: Parker, David L.  
 i REGISTRATION NUMBER: 32,165  
 i TELEPHONE: 512/418-3000  
 i TELEFAX: 512/474-7577  
 i INFORMATION FOR SEQ ID NO: 16:  
 i SEQUENCE CHARACTERISTICS:  
 i LENGTH: 134 amino acids  
 i TYPE: amino acid  
 i STRANDEDNESS:  
 i TOPOLOGY: linear

US-08-772-440-16

Query Match Score 172; DB 3; Length 134;  
 Best Local Similarity 30.7%; Pred. No. 7.e-11; Mismatches 26; Gaps 6;

Qy 25 QOKSSSSKPSCSCLVAITGLGLTAVILS-----VILCQSNSYTC--ASPS----CPD 77  
 Db 3 QEROSQKGKVCLWLWSAAVISML-----LSTCFIASCVKNGCCPN 47

Qy 78 RWKXGNHCYYSVEEKDNNSLEFCLARDSHLLVITDNEQEMSLQVFLSEAFCW-IGL- 135  
 Db 48 HWKSFSSCYLISTKENFWSTSEQNCVQMGAHLLVVTEAEQNFTQQLINESYFLGLS 107

Qy 136 --RNNSGMRWEDGSPLN 150  
 Db 108 DPQNGKQWQMDTDPFS 124

RESULT 14

US-08-543-246B-18  
 / Sequence 18, Application US/08543246B  
 / GENERAL INFORMATION:  
 / / APPLICANT: DNA and amino acid sequence specific for  
 / / TITLE OF INVENTION: natural killer cells  
 / / NUMBER OF SEQUENCES: 24  
 / / CORRESPONDENCE ADDRESS:  
 / / ADDRESSEE: Michael W. Glynn  
 / / ADDRESS: No. 6262244artis Corporation  
 / / STREET: 564 Morris Avenue  
 / / CITY: Summit,  
 / / STATE: NJ  
 / / COUNTRY: US  
 / / ZIP: 07901-1027  
 / / COMPUTER READABLE FORM:  
 / / MEDIUM TYPE: Floppy disk  
 / / COMPUTER: IBM PC compatible  
 / / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / / SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
 / / CURRENT APPLICATION DATA:  
 / / APPLICATION NUMBER: US/08/543,246B  
 / / FILING DATE:  
 / / PRIOR APPLICATION DATA:  
 / / APPLICATION NUMBER: US 07/676,663  
 / / FILING DATE: 28-MAR-1991  
 / / PRIOR APPLICATION DATA:  
 / / APPLICATION NUMBER: PCT/US92/02469  
 / / FILING DATE: 27-MAR-1992  
 / / PRIOR APPLICATION DATA:  
 / / APPLICATION NUMBER: US 08/122,514  
 / / FILING DATE: 24-SEP-1993  
 / / ATTORNEY/AGENT INFORMATION:  
 / / NAME: Kassenoff, Melvyn M.  
 / / REGISTRATION NUMBER: 26,389  
 / / REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT  
 / / TELECOMMUNICATION INFORMATION:  
 / / APPLICATION NUMBER: US 08/122,514  
 / / FILING DATE: 24-SEP-1993  
 / / ATTORNEY/AGENT INFORMATION:  
 / / NAME: Kassenoff, Melvyn M.  
 / / REGISTRATION NUMBER: 26,389  
 / / REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT  
 / / TELECOMMUNICATION INFORMATION:  
 / / TELEPHONE: 908-522-6927  
 / / TELEFAX: 908-522-6955  
 / / INFORMATION FOR SEQ ID NO: 18:  
 / / SEQUENCE CHARACTERISTICS:  
 / / LENGTH: 120 amino acids  
 / / TYPE: amino acid  
 / / STRANDEDNESS:  
 / / TOPOLOGY: linear  
 / / MOLECULE TYPE: protein  
 / / HYPOTHETICAL: NO  
 / / ANTI-S-SENSE: NO  
 / / FRAGMENT TYPE: C-terminal  
 / / US-08-543-246B-18

Query Match 72 CPSCPDRWMKYGNHCYTFSVKDWNSSLFCLARDSHLIVITDNDORMSLIQVFLSSAFC 131  
 Best Local Similarity 16.6%; Score 169.5; DB 3; Length 135;  
 Matches 37; Conservative 20; Mismatches 55; Indels 5; Gaps 3;

Db 18 CGHCPPEWITNSNCYYIGKERTWEESLLACTSKNSSLSDNEEMKFLSTIISSS-- 75

Qy 132 WIGL-RNNSGWRNEDGSPLNFSR-TISSNSPVOTCGAINKGLOSSCEVPLHGCK 185  
 Db 76 WIGVERNSSEHDWVTINGLAFKHEIIKDSDNAELNCAVLYQVNRLKSACQCGSSIIYHCK 132

Search completed: August 10, 2004, 16:35:49  
 Job time : 18 secs

RESULT 15  
 US-08-543-246B-17  
 / Sequence 17, Application US/08543246B  
 / / Patent No. 6262244  
 / / GENERAL INFORMATION:  
 / / APPLICANT: DNA and amino acid sequence specific for  
 / / TITLE OF INVENTION: natural killer cells

Qy 72 CPSCPDRWMKYGNHCYTFSVKDWNSSLFCLARDSHLIVITDNDORMSLIQVFLSSAFC 131  
 Db 3 CGHCPPEWITNSNCYYIGKERTWEESLLACTSKNSSLSDNEEMKFLSTIISSS-- 60

Qy 132 WIGL-RNNSGWRNEDGSPLNFSR-TISSNSPVOTCGAINKGLOSSCEVPLHGCK 185  
 Db 61 WIGVERNSSEHDWVTINGLAFKHEIIKDSDNAELNCAVLYQVNRLKSACQCGSSIIYHCK 117

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A;Residues: 1-146 <CHE>  
A;Cross-references: GB:AP176421  
A;Experimental source: venom gland  
A;Accession: PC7038  
A;Molecule type: protein  
A;Residues: 24-50;59-83;102-107;112-114 <CH2>  
C;Superfamily: tetranectionin; C-type lectin homology  
C;Keywords: disulfide bond; heterodimer; venom  
F;1-23/Domain: signal sequence #status Predicted <SIG>  
F;24-146/Product: agkisacutacin beta chain #status experimental <MAT>  
Query Match Score 15.9%; Best Local Similarity 30.2%; Matches 48; Conservative 15; Mismatches 71; Indels 25; Gaps 6;  
QY 35 LSRFAMYVALGILTVILSLLIMYQRLCGSKDSTSCHCPSCPILWTRNGSHCYFPMSEKK 94  
Db 1 MGRFIFVSGFLVVVF-:-----SLSGTADCPSS--EWSSEYEGHCKYKPFDEPK 44  
QY 95 DWNSSLKFCAD--KGSHLITFPDNQ---VKLFGEYLGLDFPYWGLRNI-DG--WRWEG 145  
Db 45 TWADAEKFCTQQHKCSQSHLAFHSSSEADFVTLTTPSPSKTDLYWIGLKNIWNQCYWKWSD 104  
QY 146 GPALSRLILNLSLIIORGIAIHRNGLQASSCEVALWICK 184  
Db 105 GTKLDKDWREQECLVSRVTANNNEWLSDMGGTCSFVCK 143

RESULT 3  
T2841  
C type lectin, B locus - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
R;Milne, S.; Kaufman, J.; Beck, S.  
Submitted to the EMBL Data Library, May 1998  
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex  
A;Accession: T2841  
A;Status: Preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-156 <ML>  
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PID:CAA18961.1  
A;Experimental source: clone cB12  
C;Genetics:  
A;Gene: BlcC  
A;Map position: 16  
A;Introns: 17/1; 74/3; 110/2

Query Match Score 15.1%; Best Local Similarity 25.0%; Matches 39; Conservative 24; Mismatches 68; Indels 25; Gaps 6;  
QY 39 AMVALGLITVILSLLIMYQRLCGSKDSTSCH--CPSCPILWTRNGSHCYFPMSEKK 95  
Db 3 AVFTYLTAVAFAVQAFQ-----PHPOPCAQCPCFDWGRKCYFSEDDSN 50  
QY 96 WNSSSLKFCADKGSHLITFPDNQGYLGEYLGLDFPYWGLRNI-DG--WRWEGGPALS- 150  
Db 51 WTSSQNNCSAIGASIAVDSAEDISFTMRHKGSSSHFWGLSLR-BGKEHEFWWVNRSPSLH 109  
QY 151 -LRLLTNSLIIORGCAIHRNGLQASSCEVALWICK 185  
Db 110 LFQVQGDGL--CATVGDAGLSSHCSITRRNWVCTK 142

RESULT 4  
JC4691  
coagulation factor IX/factor X-binding protein chain A precursor - habu  
C;Species: Trimeresurus flavoviridis (habu)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Jun-2000  
C;Accession: JC4691; B33332; JC4330  
R;Matsuzaki, R.; Yoshihara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Query Match Score 14.2%; Best Local Similarity 29.0%; Matches 47; Conservative 18; Mismatches 66; Indels 31; Gaps 8;  
QY 35 LSRSRPAVAGLILTVILSLLIMYQRLCGSKDSTSCHCPSCPILWTRNGSHCYFPMSEKK 94  
Db 1 MGRIFIVSGFLVVVF------SLSGTGADCPSS--WSSYEGHCKYKPFNEBK 44  
QY 95 DWNSSLKFCAD-GSHLITFPDNQ---VKLGEYLQDFPYWGLRNI--DGWRWEG 145

RESULT 5  
JC1105  
aggritin beta chain - Malayan pit viper  
C;Species: Calloselasma rhodostoma (Malayan pit viper)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 11-May-2000  
R;Chung, C.H.; Au, L.C.; Huang, T.F.  
Biochem, Biophys, Res, Commun, 263: 723-727, 1999  
A;Title: Molecular cloning and sequence analysis of aggritin, a collagen-like platelet a  
A;Accession: PC7027; PMID:99443731; PMID:10512747  
A;Molecule type: protein  
A;Residues: 1-146 <CHU>  
C;Experimental source: venom gland  
C;Superfamily: tetranectionin; C-type lectin homology  
C;Keywords: disulphide bond; platelet aggregation; venom  
Query Match Score 14.2%; Best Local Similarity 29.0%; Matches 47; Conservative 18; Mismatches 66; Indels 31; Gaps 8;  
QY 35 LSRSRPAVAGLILTVILSLLIMYQRLCGSKDSTSCHCPSCPILWTRNGSHCYFPMSEKK 94  
Db 1 MGRIFIVSGFLVVVF------SLSGTGADCPSS--WSSYEGHCKYKPFNEBK 44  
QY 95 DWNSSLKFCAD-GSHLITFPDNQ---VKLGEYLQDFPYWGLRNI--DGWRWEG 145

|                 |  |  |  |
|-----------------|--|--|--|
| Db              | 45 NWADAERFCKLQPKHSHLVSQSAAEADFFVVKLTRPRUKANLVWGMGLSNIWGCNMQWSD 104  | Db   | 107 WIGLEYSTNQNKWDNSYNSTESDNLSVMEN---RCGTPXNTKVEGDVCSGEHEHOPWVCO 162   |
| Qy              | 146 GPALSLRILTNSLIQRCGA---IHRNGHQASSCEVALQWICK 184   | Qy   | 185 K 185  |
| Db              | 105 GARLNKWDWQE- -SECLAFRGVTEWL-NMDSSTCSFVCK 143   | Db   | 163 K 163  |
| <b>RESULT 6</b> |  |  |  |
| WNVZF2          | hepatic lectin homolog (BamHI-ORF2) - fowlpox virus (isolate HP-438 [Munich])<br>C;Species: Fowlpox virus<br>C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000<br>C;Accession: B29963<br>R;Tomley, F.; Bains, M.; Campbell, J.; Bourneill, M.<br>J. Gen. Virol. 69, 1025-1040, 1988<br>A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox<br>A;Reference number: UT0442; PMID:8829622; PMID:2836548<br>A;Accession: B29963   | Query Match 13.4%; Score 138; DB 1; Length 167;<br>Best Local Similarity 27.1%; Pred. No. 3.7e-06;<br>Matches 38; Conservative 28; Mismatches 62; Indels 12; Gaps 4;   | Query Match 13.1%; Score 135; DB 2; Length 144;<br>Best Local Similarity 25.5%; Pred. No. 6.3e-06;<br>Matches 36; Conservative 23; Mismatches 64; Indels 18; Gaps 5;   |
| Qy              | 35 LSRPAMVALGLLTIVLMSLIMYORILCCSKDSTCSCSPCLILWTRNGSHCYFSMEK 94   | Qy   | 66 DSTOSHCPSCPILWTRNGSHCYFSMEKDDWNSLKLKEC--ADKGSHLITFPDNQGVKLFG 123  |
| Db              | 12 VSCCAITVPGILCLILFTP...-WVTKRKYIAPYFKVCPEWIGGNKCYFTINE 68  | Db   | 4 EGTRAGLEDCDFSWPSYDQHQCQAQNSEQKTWEAEKFRAENGHAHLASIESNGEADFVS 63   |
| Qy              | 95 DWNSSLKPCADKGSHLITPDNGQYKLFSEYLQDFYWLGL---RNTDGWRW---EGG 146  | Qy   | 124 -----BYLGODDEWYIGLNRID---GWRWEGGPALSRLRILTSLITQRCGAIR-NGL 170  |
| Db              | 69 NWNDSSKCLDVMDSLRLDNTINRKTPEINFSLYYEGV 127   | Db   | 64 WLISQKDELADEEYWIGRAQNKEQQCSSENSDGSSVSYENLIDLHTKKCGALEKLTF 123   |
| Qy              | 147 PALSRLITNSLIQRCGAH 166   | Qy   | 171 QA---SSCEVALQWICKKVY 188   |
| Db              | 128 NDICLFLFDNSNITEMSCIFH 147  | Db   | 124 RKNVNNYYCBOMEAFFVCKLDPY 144  |
| <b>RESULT 7</b> |  |  |  |
| T28140          | natural killer cell receptor homolog - chicken (fragment)<br>C;Species: Gallus gallus (chicken)<br>C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999<br>C;Accession: T28140<br>R;Milne, S.; Kaufman, J.; Beck, S.<br>submitted to the EMBL Data Library, May 1998<br>A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex<br>A;Reference number: Z20475<br>A;Accession: T28140<br>A;Status: preliminary; translated from GB/EMBL/DDJB<br>A;Molecule type: DNA<br>A;Residues: 1-170 <MIL>   | Query Match 13.3%; Score 136.5; DB 2; Length 170;<br>Best Local Similarity 25.6%; Pred. No. 5.3e-06;<br>Matches 31; Conservative 16; Mismatches 63; Indels 11; Gaps 3; | Query Match 13.5%; Score 136.5; DB 2; Length 170;<br>Best Local Similarity 25.6%; Pred. No. 5.3e-06;<br>Matches 31; Conservative 16; Mismatches 63; Indels 11; Gaps 3; |
| Qy              | 72 CPSCPILWTRNGSHCYFSMEKDDWNSLKLKECADCYGSHLITFPDNQGVKLFGEVIGQDFY 131   | Qy   | 72 CPLLCPQFWRLGDRCYELSTEKGNTQAMKMCENIQSQAVLRKKAEDHLQQMAGAEV 106  |
| Db              | 47 CLLCPQFWRLGDRCYELSTEKGNTQAMKMCENIQSQAVLRKKAEDHLQQMAGAEV 106   | Qy   | 132 WIGLR-NIDGMRWEGGPAL-----SLRLTNTSLLQRCGAIRNGLQASSCEVALQWICK 184   |
| <b>RESULT 8</b> |  |  |  |
| PC7027          | aggregatin alpha chain - Malayan pit viper (fragment)<br>C;Species: Calloselasma rhodostoma (Malayan pit viper)<br>C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000<br>C;Accession: PC7027<br>R;Cheng, C.H.; Au, L.C.; Huang, T.F.<br>Blochem. Biophys. Res. Commun. 263, 723-727, 1999<br>A;Title: Molecular cloning and sequence analysis of aggregatin, a collagen-like platelet ε   | Query Match 13.1%; Score 135; DB 2; Length 144;<br>Best Local Similarity 25.5%; Pred. No. 6.3e-06;<br>Matches 36; Conservative 23; Mismatches 64; Indels 18; Gaps 5;   | Query Match 13.1%; Score 135; DB 2; Length 144;<br>Best Local Similarity 25.5%; Pred. No. 6.3e-06;<br>Matches 36; Conservative 23; Mismatches 64; Indels 18; Gaps 5;   |
| Qy              | 146 GPALSLRILTNSLIQRCGA---IHRNGHQASSCEVALQWICK 184   | Qy   | 66 DSTOSHCPSCPILWTRNGSHCYFSMEKDDWNSLKLKEC--ADKGSHLITFPDNQGVKLFG 123  |
| Db              | 105 GARLNKWDWQE- -SECLAFRGVTEWL-NMDSSTCSFVCK 143   | Db   | 4 EGTRAGLEDCDFSWPSYDQHQCQAQNSEQKTWEAEKFRAENGHAHLASIESNGEADFVS 63   |
| <b>RESULT 9</b> |  |  |  |
| A47267          | bhorocetin alpha chain - jararaca<br>N;Alternate names: two chain bhorocetin alpha chain<br>C;Species: Bothrops jararaca (jararaca)<br>C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998<br>C;Accession: A47267; B37958<br>R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.<br>Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993<br>A;Title: Primary structure of two-chain bhorocetin, a von Willebrand factor modulator protein<br>A;Reference number: A47267; MUID:93157385; PMID:8430107<br>A;Accession: A47267<br>A;Molecule type: protein<br>A;Residues: 1-133 <USA><br>A;Experimental source: venom<br>A;Note: sequence extracted from NCBI backbone (NCBIP:124085)<br>R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Ohama, R.; Matsui, T.; Fukui, H.; Suzuki, M.; Ochiai, K.; Titani, K.<br>Bichemistry 30, 1957-1964, 1991<br>A;Title: Isolation and chemical characterization of two structurally and functionally distinct chains<br>A;Reference number: A37958; MUID:91129280; PMID:91129280<br>A;Accession: B37958<br>A;Molecule type: protein<br>A;Residues: 1-133 <USA> | Query Match 11.6%; Score 119; DB 2; Length 133;  | Query Match 11.6%; Score 119; DB 2; Length 133;  |
| Qy              | 72 CPLLCPQFWRLGDRCYELSTEKGNTQAMKMCENIQSQAVLRKKAEDHLQQMAGAEV 106  | Qy   | 132 WIGLR-NIDGMRWEGGPAL-----SLRLTNTSLLQRCGAIRNGLQASSCEVALQWICK 184   |

Best Local Similarity 25.4%; Pred. No. 0.00021;  
Matches 29; Conservative 26; Mismatches 33; Indels 26; Gaps 7;

Qy 75 CPILWTRNGSHCYYSMEKQDNSSLKFCAD--KGSHLLTPDNOQYKLFG--EYLG-- 127  
Db 2 CPSGWSSYEGNCYKPFQQMKNDAEFPFCSEQAKGGHLSV----TKIYSEKEKDFVGDL 55

Qy 128 ----QDFY-WIGLR-NLD---GWRGEPPALSLRILNTSILQRCGATHRN 168  
Db 56 VTKNIQSSDLIYAWIGLRFENKEKQCSSEWDGSSSVSYENVERTVKKCPALEKD 109

RESULT 10  
B42972 coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper  
C;Species: Vipera russelli (Russell's viper)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Feb-1997  
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.  
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no  
A;Reference number: A42972; MUID:92332516; PMID:1629211  
A;Contents: V. r. siamensis  
A;Accession: B42972  
A;Status: Preliminary  
A;Molecule type: protein  
A;Residues: 1-123 <MRK>  
A;Experimental source: venom  
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)  
C;Superfamily: tetratocetin; C-type lectin homology  
C;Keywords: hydrolase; metalloproteinase; venom; zinc  
F;4-121/Domain: C-type lectin homology <LCH>  
F;4-15,32-121,98-113/Disulfide bonds: #status predicted

Query Match 11.4%; Score 117.5; DB 2; Length 123;  
Best Local Similarity 26.4%; Pred. No. 0.00027;  
Matches 32; Conservative 15; Mismatches 61; Indels 13; Gaps 4;

Qy 75 CPILWTRNGSHCYYSMEKQDNSSLKFCAD--KGSHLLTPDNOQ---VKLFGHYLQG 128  
Db 4 CPSGWSSYEQCCKGNDLKNWDAEKPCTEQKGKSHLVSREEEFVNLLSENLEY 63

Qy 129 DFWIGLNRIDGWR---WEGGPAALSLRILNTSILQRCGAIRHNLQASSECAVLQWIC 183  
Db 64 PATWIGLGNM--WKDERMENSDRGNYKVALAEESVCLIMITHEKWSWTCNFTAPPVC 121

Qy 184 K 184  
Db 122 K 122

RESULT 11  
JC7134 agkisacutacin alpha chain precursor - sharp-nosed viper  
N;Alternative names: fibrinogenlytic venom protein  
C;Species: Agkistrodon acutus (sharp-nosed viper)  
C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000  
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.  
Biochem Biophys Res Commun. 265, 530-535, 1999  
A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom  
A;Reference number: JC7134; MUID:20025379; PMID:1058303  
A;Accession: JC7134  
A;Molecule type: protein  
A;Residues: 1-152 <CHE>  
A;Cross-references: GB:AF176420  
A;Experimental source: venom gland  
A;Accession: PC7037  
A;Molecule type: protein  
A;Residues: 24-53;84-97;125-136;137-152 <CH2>  
C;Superfamily: tetratocetin; C-type lectin homology  
C;Keywords: disulfide bond; heterodimer; venom  
F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>  
Query Match 11.1%; Score 114.5; DB 2; Length 152;  
Best Local Similarity 23.6%; Pred. No. 0.00067;  
Matches 35; Conservative 18; Mismatches 60; Indels 35; Gaps 6;

Qy 35 LSRPAMYVALGLTIVLMSLMLYMRILLCGSKSDSTCSHCPSCPSPILWTRNGSHCYFSMEKK 94  
Db 1 MGRFLTVSGFLVIVEL----SLSGTAADCSSG----WSEYEGCYKVPKQSK 44

Qy 95 DWNSLRLKFCADK-GSHLLTPDPDNQVKLFRGEYLQDF----YWIGLR----NI 138  
Db 45 TWADASEFCRKVQNGHLVLESSGEADFYAHLLAQIKSAKITHWIGLRAQNKEKQCSI 104

RESULT 12  
B42767 botrocetin beta chain - jararaca  
N;Alternative names: two chain botrocetin beta chain  
C;Species: Bothrops jararaca (jararaca)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-May-1998  
C;Accession: BA7267; C37958

R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993  
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator protein  
A;Reference number: A47267; MUID:93157385; PMID:8430107  
A;Accession: B42767  
A;Molecule type: protein  
A;Residues: 1-125 <USA>  
A;Experimental source: venom  
A;Note: sequence extracted from NCBI backbone (NCBIP:124086)  
R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su  
Biochemistry 30, 1957-1964, 1991  
A;Title: Isolation and chemical characterization of two structurally and functionally different  
A;Reference number: A37958; MUID:91129200; PMID:91129200  
A;Accession: C37958  
A;Molecule type: protein  
A;Residues: 1-40 <FOU>  
C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains  
C;Superfamily: tetranectin; C-type lectin homology  
C;Keywords: hemaglutinin; heterodimer; venom  
F;2-121/Domain: C-type lectin homology <LCH>  
F;2-13,30-121,98-113/Disulfide bonds: #status experimental  
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 11.0%; Score 113.5; DB 2; Length 125;  
Best Local Similarity 31.3%; Pred. No. 0.00069;  
Matches 26; Conservative 12; Mismatches 32; Indels 13; Gaps 4;

Qy 75 CPILWTRNGSHCYYSMEKQDNSSLKFCADK-GSHLLTPDPDNQSV---KLFGHYLQG 128  
Db 2 CPPDMSSYEGCYRFFKEWMMHDAAEFTCEQQTAHLVFSQSKEEADFVRSLTSEMLKG 61

Qy 129 DFWIGLNRIDGWR---RMEGG 146  
Db 62 DWWIGLSDV--WNKCRFENTDG 82

RESULT 13  
S78774 perlucin - Haliotis laevigata  
C;Species: Haliotis laevigata  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 17-Mar-2000  
C;Accession: S78774  
R;Mann, K.  
submitted to the Protein Sequence Database, January 2000  
A;Reference number: S78774  
A;Content: S78774  
A;Accession: S78774